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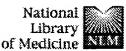
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Γ	L29	L28 AND tyrosine kinase	128			
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	L26	hGrb14	0			
	L25	L24 AND insulin receptor	45			
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	L21	L20 AND insulin receptor	23			
	L20	L18 AND PIR	165			
	L19	L18 AND hGrb14	0			
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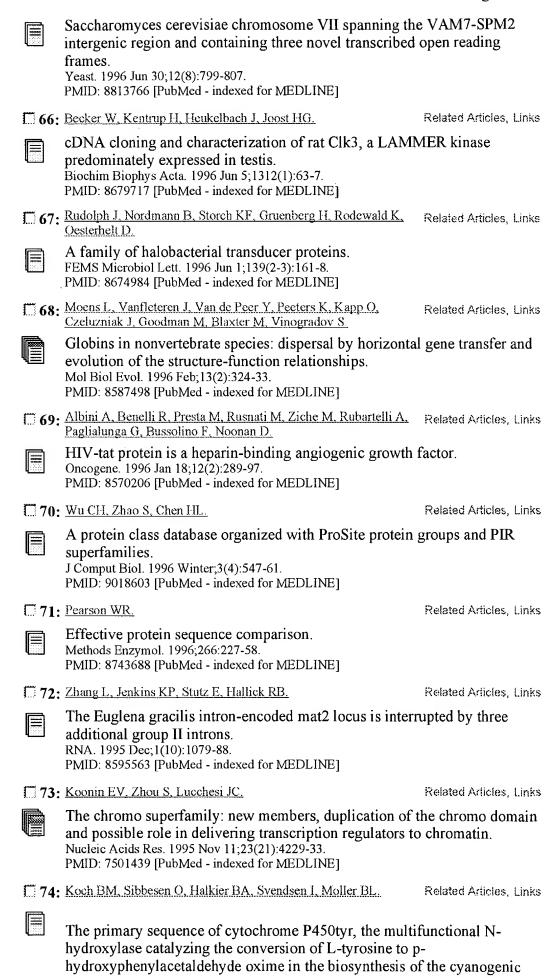
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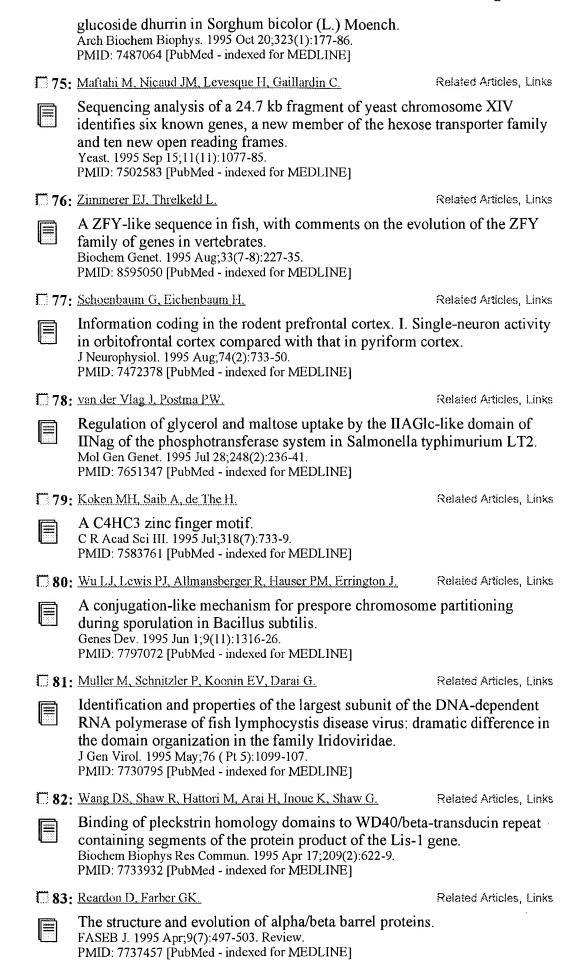
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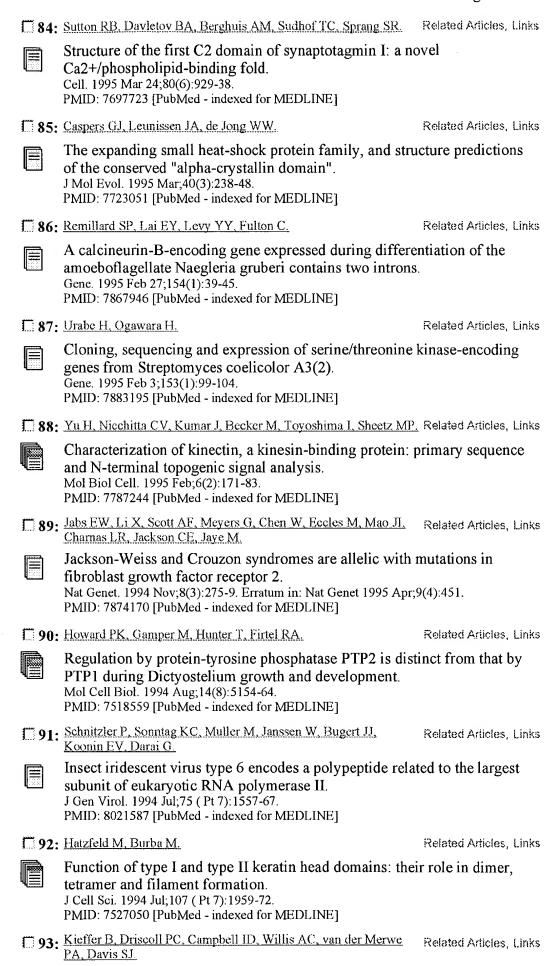
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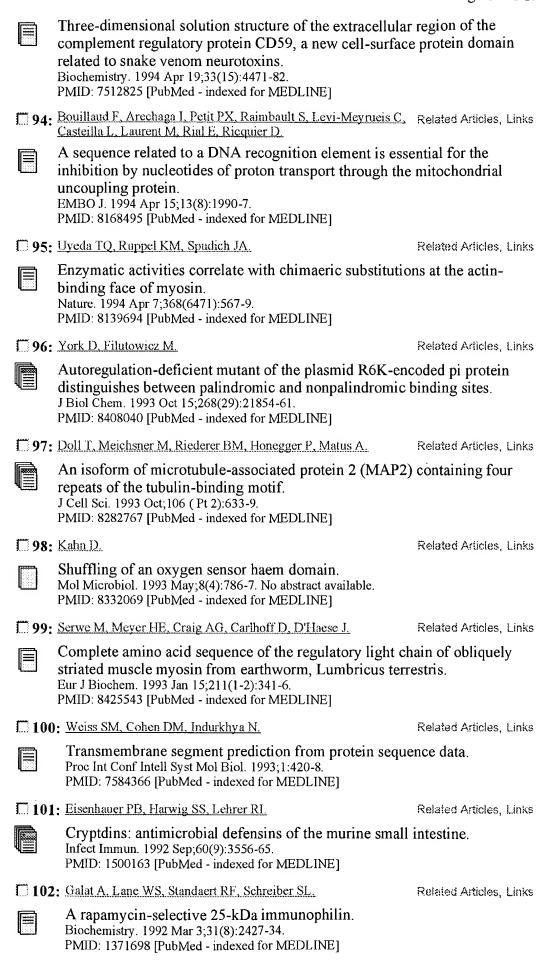




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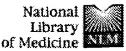
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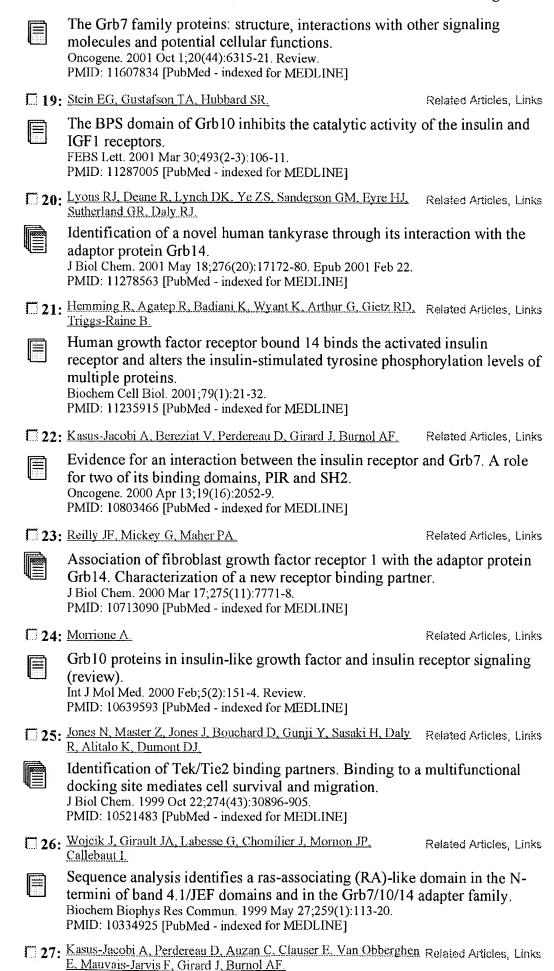
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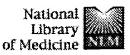
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                               20021112
                         Α
     US 2002-425256P
                         Ρ
                              20021112
     WO 2002-US38216
                              20021112
                         Α
     WO 2002-US38222
                              20021112
                         Α
     US 2003-448461P
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                              20030221
     US 2003-448462P
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     US 2003-457877P
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                              20030331
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AN
     2004:311060
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DN
     140:333607
     Differentially nucleic acids and encoded proteins useful for diagnosing
ΤI
     testicular seminomas
IN
     Nakamura, Yusuke; Katagiri, Toyomasa
     Oncotherapy Science, Inc., Japan; Japan as Represented by the President of
PA
     the University of Tokyo
SO
     PCT Int. Appl., 120 pp.
     CODEN: PIXXD2
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LA
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              LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM,
              PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU
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PRAI US 2002-414677P
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TI
      Balmer Lois (AU); Leedman Peter J (AU); Thomson Andrew (AU)
IN
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PA
                       A1 20040624
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      US 2000-168781
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                                       PCT 371 date
                            20001222
                                       PCT 102(e) date
      AU 1999-4835
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      US 2004121323
                            20040624
FΙ
      Utility; Patent Application - First Publication
DT
FS
      CHEMICAL
      APPLICATION
CLMN
      14
GΙ
       16 Figure(s).
     FIG. 1 shows a schematic of the Grb7 family members.
     FIG. 2A, FIG. 2B, FIG. 2C, FIG. 2D, FIG. 2E and FIG. 2F show regulation of
      EGF-R mRNA expression by EGF in MDA-468 and BT-20 human breast cancer
      cells, including Northern, Western blot and actinomycin D chase assays.
     FIG. 3A, FIG. 3B, FIG. 3C, FIG. 3D, FIG. 3E, FIG. 3F, FIG. 3G and FIG. 3H
      show a schematic of EGF-R mRNA, the clones generated for transfection and
      RNA electrophoretic gel mobility shift assay (REMSA), as well as data
      from transfections and cell free mRNA decay assay.
     FIG. 4A, FIG. 4B, FIG. 4C, FIG. 4D and FIG. 4E show results of multiple transfections into breast cancer cells, and assays of mRNA decay using
      the LightCycler.
     FIG. 5A and FIG. 5B show REMSA and UV cross-linking assays with a variety
      of cell extracts and riboprobes.
     FIG. 6A and FIG. 6B show specificty of binding for the EGF-R mRNA probe
      used as bait in the yeast three-hybrid screening.
     FIG. 7A, FIG. 7B, FIG. 7C and FIG. 7D show REMSA using sense and antisense
      DNA oligomers, as well as RNA probe mutants to define the RNA binding
      site within the EGF-R bait.
     FIG. 8A, FIG. 8B and FIG. 8C show a schematic of the yeast threehybrid
      screening method, REMSA with Grb7 and other antibodies as well as a UV
      cross-linking Western assay using Grb7 antibodies (SenGupta et al.,
      1996).
     FIG. 9A shows a schematic illustrating the amino acid homology between the
      Grb7 family members and the KH-motif. FIG. 9B and FIG. 9C show the
      predicted secondary structure of the Grb7 mRNA binding motif.
     FIG. 10A and FIG. 10B show a schematic of Grb7 family member GSTfusion
      proteins, a REMSA using GST-Grb7 fusion protein with EGFR mRNA and REMSA
      with unlabeled RNA competitors.
     FIG. 11A, FIG. 11B, FIG. 11C, FIG. 11D, FIG. 11E and FIG. 11F show a schematic of the GST-Grb7 mutants, REMSA using the Grb7 mutants with
      EGF-R 2/2A riboprobe and REMSA with different EGFR mRNA probes with each
      of the mutants demonstrating RNA specificity.
     FIG. 12A and FIG. 12B show the sequence of the erbB-2 riboprobe used, and
      a REMSA showing binding of Grb7 and Grb10 to erbB-1 and erbB-2 mRNA.
     FIG. 13A and FIG. 13B show REMSA binding of Grb7 and two mutants to EGF-R
      and erbB-2 mRNAs, together with sequence comparisons and stem-loop plots
      of the RNA structures.
     FIG. 14A and FIG. 14B show binding by GST-Grb10 and GST- ***Grb14***
      erbB-2 mRNA. A competition REMSA with tRNA using Grb7-M3 mutant confirmed
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specificity to the erbB-2 mRNA probe.

DT

Patent

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EGF-R primers and a western blot of EGF-R levels in cells overexpressing
       Grb7,
      FIG. 16 shows an actinomycin D chase to determine the rate of EGF-R mRNA
       decay in stably transfected MDA-468 cells that overexpress Grb7.
L2
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AN
      2004:449883 CAPLUS
      140:402911
DN
      Binary prediction tree modeling with many predictors and its uses in
TI
      clinical and genomic applications
IN
      Nevins, Joseph R.; West, Mike; Huang, Andrew T.
PA
      Duke University, USA
      PCT Int. Appl., 886 pp.
SO
      CODEN: PIXXD2
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L2
     ANSWER 6 OF 156 USPATFULL ON STN
AN
        2004:50778 USPATFULL
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        Gene expression in bladder tumors
ΙN
        Orntoft, Torben F., Aabyhoj, DENMARK
PT
        US 2004038207
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                                     20010914 (9)
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        Division of Ser. No. US 2000-510643, filed on 22 Feb 2000, UNKNOWN
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        NCLM: 435/006.000
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.
     ANSWER 7 OF 156 USPATFULL ON STN
12
        2004:24686 USPATFULL
AN
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FIG. 15A and FIG. 15B show immunoprecipitation reverse transcriptase polymerase chain reaction (IP-RT-PCR) assay using Grb7 antibodies and

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TI
        Methods and compositions for the prediction, diagnosis, prognosis,
        prevention and treatment of malignant neoplasma
        Wirtz, Ralph, Koln, GERMANY, FEDERAL REPUBLIC OF
IN
        Munnes, Marc, Erkrath, GERMANY, FEDERAL REPUBLIC OF Kallabis, Harald, Koln, GERMANY, FEDERAL REPUBLIC OF
        Bayer Aktiengesellschaft, Leverkusen, GERMANY, FEDERAL REPUBLIC OF, D
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        51368 (non-U.S. corporation)
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        US 2004018525
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                                     20040129
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        EP 2003-3112
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.
      ANSWER 8 OF 156 USPATFULL ON STN
L2
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AN
ΤI
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        Guo, Xiaojia, Branford, CT, UNITED STATES
IN
        Fernandes, Elma, Branford, CT, UNITED STATES
Li, Li, Branford, CT, UNITED STATES
Kekuda, Ramesh, Stamford, CT, UNITED STATES
        Liu, Yi, New Haven, CT, UNITED STATES
        Leite, Mario, Milford, CT, UNITED STATES
        Spytek, Kimberly A., New Haven, CT, UNITED STATES
        Ji, Weizhen, Branford, CT, UNITED STATES
        Casman, Stacie J., North Haven, CT, UNITED STATES
        Boldog, Ference L., North Haven, CT, UNITED STATES Patturajan, Meera, Branford, CT, UNITED STATES Vernet, Corine A. M., Branford, CT, UNITED STATES
        Ballinger, Robert A., Newington, CT, UNITED STATES Malyankar, Uriel M., Branford, CT, UNITED STATES
        Tchernev, Velizar T., Branford, CT, UNITED STATES
        Blalock, Angela D., Branford, CT, UNITED STATES
        Gusev, Vladimir Y., Madison, CT, UNITED STATES
Rastelli, Luca, Guilford, CT, UNITED STATES
        Mezes, Péter D., Old Lymé, CŤ, UNITED STATES
Ellerman, Karen, Branford, CT, UNITED STATES
        Heyes, Melvyn, New Haven, CT, UNITED STATES
        Herrmann, John L., Guilford, CT, UNITED STATES Shimkets, Richard A., Guilford, CT, UNITED STATES
        Ioime, Noelle, Hamden, CT, UNITED STATES
        Pena, Carol E. A., New Haven, CT, UNITED STATES
        Shenoy, Suresh G., Branford, CT, UNITED STATES
        Taupier, Raymond J., JR., East Haven, CT, UNITED STATES
        Gerlach, Valerie, Branford, CT, UNITED STATES
        Gorman, Linda, East Haven, CT, UNITED STATES
PΙ
                                      20040115
        US 2004010119
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20010213 (60)
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        US 2001-268496P
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        US 2001-335104P
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        US 2001-335109P
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20011121 (60)

US 2001-332127P

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20011121 (60)
        US 2001-331772P
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        INCLS: 514/012.000; 435/006.000; 435/069.100; 435/320.100; 435/325.000;
                536/023.200
                530/350.000
NCL
        NCLM:
                514/012.000; 435/006.000; 435/069.100; 435/320.100; 435/325.000;
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                536/023.200
IC
        [7]
        ICM: C12Q001-68
        ICS: C07H021-04; A61K038-17; C07K014-435; C07K014-47; C12P021-02;
        C12N005-06
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
12
     ANSWER 9 OF 156 CAPLUS COPYRIGHT 2004 ACS ON STN DUPLICATE 5
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AN
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     Regulation and functional roles of
ΤI
     Cariou, Bertrand; Bereziat, Veronique; Moncoq, Karine; Kasus-Jacobi, Anne;
ΑU
      Perdereau, Dominique; Le Marcis, Veronique; Burnol, Anne-Francoise
     Dep. Endocrinol., Inst. Cochin INSERM U 567-CNRS UMR 8104, Univ. Rene
CS
     Descartes, Paris, 75014, Fr. Frontiers in Bioscience (2004), 9(2), 1626-1636
SO
      CODEN: FRBIF6; ISSN: 1093-4715
     URL: http://www.bioscience.org/2004/v9/af/1228/pdf.pdf
PR
      Frontiers in Bioscience
      Journal; (online computer file)
DT
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LA
     ANSWER 10 OF 156 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
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     The Genuine Article (R) Number: 779ZA
GA
      Regulation and functional roles of ***Grb14***
TI
      Cariou B; Bereziat V; Moncoq K; Kasus-Jacobi A; Perdereau D; Le Marcis V;
ΑU
      Burnol A F (Reprint)
     Univ Paris 05, CNRS, UMR 8104, Dept Endocrinol, INSERM, U567, Inst Cochin, F-75014 Paris, France (Reprint); Fac Pharm Paris V, Lab Cristallog & RMN
      Biol, F-75006 Paris, France
CYA
      FRONTIERS IN BIOSCIENCE, (MAY 2004) Vol. 9, pp. 1626-1636.
      Publisher: FRONTIERS IN BIOSCIENCE INC, C/O NORTH SHORE UNIV HOSPITAL,
      BIOMEDICAL RESEARCH CENTER, 350 COMMUNITY DR, MANHASSET, NY 11030 USA.
      ISSN: 1093-9946.
      Article; Journal
DT
      English
LA
REC
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12
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AN
TI
      Increased adipose tissue expression of
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      of insulin resistance
AU
      Carfiou, Bertrand; Capitaine, Nadege; Le Marcis, Veronique; Vega
     Nathalie; Bereziat, Veronique; Kergoat, Micheline; Laville, Martine; Girard, Jean; Vidal, Hubert; Burnol, Anne-Francoise Dep. d'Endocrinol., Inst. Cochin INSERUM U 567-CNRS UMR 8104, Univ. Rene Descartes, Paris, 75674, Fr. FASEB Journal (2004), 18(9), 965-967, 10.1096/fj.03-0824fje CODEN: FAJOEC; ISSN: 0892-6638
CS
SO
PB
      Federation of American Societies for Experimental Biology
DT
      Journal
      English
LA
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        36
                THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT
      ANSWER 12 OF 156
                              MEDLINE on STN
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AN
      PubMed ID: 15059968
DN
TI
      Increased adipose tissue expression of
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      of insulin resistance.
      Cariou Bertrand; Capitaine Nadege; Le Marcis Veronique; Vega Nathalie;
      Bereziat Veronique; Kergoat Micheline; Laville Martine; Girard Jean; Vidal
      Hubert; Burnol Anne-Francoise
      Departement d'Endocrinologie, Institut Cochin INSERM U 567-CNRS UMR
CS
      8104-Universite Rene Descartes, Paris, France.
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S0
     FASEB journal : official publication of the Federation of American
     Societies for Experimental Biology, (2004 Jun) 18 (9) 965-7.
     Journal code: 8804484. ISSN: 1530-6860.
CY
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     Journal; Article; (JOURNAL ARTICLE)
DT
LA
     English
     IN-PROCESS; NONINDEXED; Priority Journals
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     Last Updated on STN: 20040608
L2
     ANSWER 13 OF 156 CAPLUS COPYRIGHT 2004 ACS ON STN DUPLICATE 6
     2004:114768 CAPLUS
AN
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DN
TI
     Grb10 exceeding the boundaries of a common signaling adapter
ΑU
     Riedel, Heimo
     Department of Biological Sciences, Wayne State University, Detroit, MI,
     48202, USA
     Frontiers in Bioscience (2004), 9(1), 603-618
SO
     CODEN: FRBIF6; ISSN: 1093-4715
     URL: http://www.bioscience.org/2004/v9/af/1227/pdf.pdf
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     Frontiers in Bioscience
     Journal; General Review; (online computer file)
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     Riedel H (Reprint)
ΑU
     Wayne State Univ, Dept Biol Sci, 2171 BSB, Detroit, MI 48202 USA
CS
     (Reprint); Wayne State Univ, Dept Biol Sci, Detroit, MI 48202 USA
CYA
     FRONTIERS IN BIOSCIENCE, (JAN 2004) Vol. 9, pp. 603-618. Publisher: FRONTIERS IN BIOSCIENCE INC, C/O NORTH SHORE UNIV HOSPITAL,
S0
     BIOMEDICAL RESEARCH CENTER, 350 COMMUNITY DR, MANHASSET, NY 11030 USA.
     ISSN: 1093-9946.
DT
     General Review; Journal
     English
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     Reference Count: 105
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     ANSWER 15 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
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     2004:244934
                   BIOSIS
     PREV200400246629
DN
TT
     Improved glucose homeostasis and enhanced insulin signalling in
        ***Grb14***
                    -deficient mice.
     Cooney, Gregory J.; Lyons, Ruth J.; Crew, A. Jayne; Jensen, Thomas E.;
     Molero, Juan Carlos; Mitchell, Christopher J.; Biden, Trevor J.; Ormandy,
     Christopher J.; James, David E.; Daly, Roger J. [Reprint Author]
     Cancer Research Program, Garvan Institute of Medical Research, 384
CS
     Victoria St, Sydney, NSW, 2010, Australia
     r.daly@garvan.org.au
     EMBO (European Molecular Biology Organization) Journal, (11 February 2004) Vol. 23, No. 3, pp. 582-593. print. ISSN: 0261-4189 (ISSN print).
S0
     Article
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ED
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     Last Updated on STN: 6 May 2004
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     ANSWER 16 OF 156 CAPLUS COPYRIGHT 2004 ACS ON STN DUPLICATE 8
     2004:114729 CAPLUS
AN
DN
     140:214448
TI
     Grb10: more than a simple adaptor protein
     Lim, Mei A.; Riedel, Heimo; Liu, Feng
ΑU
     Department of Pharmacology, University of Texas Health Science Center at
     San Antonio, San Antonio, TX, 78229, USA
Frontiers in Bioscience (2004), 9(1), 387-403
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     URL: http://www.bioscience.org/2004/v9/af/1226/pdf.pdf
     Frontiers in Bioscience
     Journal; General Review; (online computer file)
DT
     English
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      2004:114784 CAPLUS
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      GRB7 in intracellular signaling and its role in cell regulation
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ΑU
     Shen, Tang-Long; Guan, Jun-Lin
     Department of Molecular Medicine, Cornell University, Ithaca, NY, 14853,
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      Frontiers in Bioscience (2004), 9(1), 192-200
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      Journal; General Review; (online computer file)
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     Cariou, Bertrand; Capitaine, Nadege; Le Marcis, Veronique; Vega, Nathalie; Bereziat, Veronique; Kergoat, Micheline; Laville, Martine; Girard, Jean;
ΑU
     Vidal, Hubert; Burnol, Anne- Francoise [Reprint Author]
CS
      CNRSUMR 8104INSERM, U567, Inst Cochin, Dept Endocrinol, Univ Paris 05,
      F-75674, Paris, France
      burnol@cochin.inserm.fr
SO
     FASEB Journal, (April 2004) Vol. 18, No. 6, pp. NIL_0336-NIL_0356. print.
     ISSN: 0892-6638 (ISSN print).
DT
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     English
LA
     Entered STN: 9 Jun 2004
ED
     Last Updated on STN: 9 Jun 2004
L2
     ANSWER 19 OF 156 SCISEARCH COPYRIGHT 2004 THOMSON ISI ON STN
ΑN
     2004:415366 SCISEARCH
     The Genuine Article (R) Number: 816KM
GΑ
                                                    ***Grb14***
TI
     Increased adipose tissue expression of
                                                                    in several models
     of insulin resistance
     Cariou B; Capitaine N; Le Marcis V; Vega N; Bereziat V; Kergoat M; Laville M; Girard J; Vidal H; Burnol A F (Reprint)
Univ Paris 05, CNRS, UMR 8104, INSERM, U567, Inst Cochin, Dept Endocrinol, F-75674 Paris, France (Reprint); Fac Med R Laennec, Ctr Rech & Nutr
ΑU
CS
     Humaine Lyon, Lyon, France; Hop Edouard Herriot, Serv Endocrinol Diabetol
     & Nutr, Lyon, France
CYA
     France
SO
     FASEB JOURNAL, (APR 2004) Vol. 18, No. 6.
     Publisher: FEDERATION AMER SOC EXP BIOL, 9650 ROCKVILLE PIKE, BETHESDA, MD
     20814-3998 USA.
     ISSN: 0892-6638.
DT
     Article; Journal
LA
     English
REC
     Reference Count: 36
     *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
L2
     ANSWER 20 OF 156 DISSABS COPYRIGHT (C) 2004 ProQuest Information and
     Learning Company; All Rights Reserved on STN
AN
     2003:43622 DISSABS
                              Order Number: AAI3075524
ΤI
     Structural and functional analysis of the BPS and SH2 domains of Grb10
ΑU
     Stein, Evan Gary [Ph.D.]; Hubbard, Stevan R. [advisor]
     New York University (0146)
CS
     Dissertation Abstracts International, (2003) Vol. 63, No. 12B, p. 5687. Order No.: AAI3075524. 91 pages.
SO
     ISBN: 0-493-95827-4.
DT
     Dissertation
FS
     DAI
LA
     English
L2
      ANSWER 21 OF 156 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
      DUPLICATE 10
AN
      2004-01504 BIOTECHDS
ΤI
      Screening for drugs using altered expression of specified genes in
```

frontal lobe or hippocampus of depression model animal, and diagnosis of

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depression;
           animal model and biochip for use in drug screening and disease therapy
PA
       RIKAGAKU KENKYUSHO
       JP 2003274949 30 Sep 2003
PΙ
       JP 2002-81502 22 Mar 2002
ΑI
       JP 2002-81502 22 Mar 2002; JP 2002-81502 22 Mar 2002
PRAI
DT
       Patent
LA
       Japanese
       WPI: 2003-822458 [77]
os
L2
      ANSWER 22 OF 156 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 11
       10399185 IFIPAT; IFIUDB; IFICDB
AN
       DIAGNOSIS OF DISEASES ASSOCIATED WITH THE IMMUNE SYSTEM BY DETERMINING
TI
       CYTOSINE METHYLATION
       Berlin Kurt (DE); Olek Alexander (DE); Piepenbrock Christian (DE)
Unassigned Or Assigned To Individual (68000)
IN
PA
PΙ
       us 2003143606
                          A1 20030731
       us 2002-311455
                                20021216
ΑI
       WO 2001-EP7537
                                20010702
                                20021216
                                            PCT 371 date
                                20021216
                                            PCT 102(e) date
PRAI
       DE 2000-10032529
                                20000630
       DE 2000-10043826
                                20000901
       us 2003143606
                                20030731
DT
       Utility; Patent Application - First Publication
FS
       CHEMICAL
       APPLICATION
CLMN
      ANSWER 23 OF 156 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 12
L2
       10385219 IFIPAT; IFIUDB; IFICDB
ΑN
TI
       GDU, A NOVEL SIGNALLING PROTEIN
       Daly Roger John (AU); Sutherland Robert Lyndsay (AU)
Unassigned Or Assigned To Individual (68000)
US 2003129639 A1 20030710
IN
PA
PΙ
       US 2002-323001
AΙ
                                20021218
       WO 1996-AU258
RLI
                                19960502 Section 371 PCT Filing UNKNOWN
       US 1998-945771
                                19980422 DIVISION
       US 2002-242332
                                20020911 DIVISION
       AU 1995-2742
PRAI
                                19950502
       US 2003129639
                                20030710
FΙ
       us 6465623
DT
       Utility; Patent Application - First Publication
FS
       CHEMICAL
       APPLICATION
CLMN
        3 Figure(s).
GΙ
                                                              ***Grb14***
      FIG. 1 shows a schematic representation of
                                                                               structure with
       a restriction map for the ***Grb14*** cDNA and the cDNA clones used to derive the ***Grb14*** sequence aligned underneath. The initial
       clone isolated by CORT screening was designated clone 1. Two other clones
       (1-1 and 1-2) were isolated from the 184 cell line library by screening
       using clone_1 as a probe. The ***Grb14***
                                                               CDNA sequence was completed
       using two clones L5 and L6, isolated from a human liver cDNA library.
      Abbreviations are as follows: A; Apa I; Av; Avr II, X; Xho I; E; Eco RI. The numbers refer to distance in bp.
FIG. 2 shows the nucleotide and amino acid sequence of ***Grb14***.
       The PH domain is underlined and the SH2 domain indicated by bold type.
       The translation termination codon is shown by an asterisk in the amino
       acid sequence. Numbers refer to distances in bp.
      FIG. 3 shows the sequence homology between
       and F10E9.6. As alignment of the amino acid sequences of ***Grb14***
       mouse Grb7, mouse Grb10 and C. elegans F10E9.6 was obtained using the
       computer programs Clustal W and SeqVu. Identical residues are boxed. A highly conserved proline-rich motif is indicated by the dotted underline, the PH domain by the broken underline and the SH2 domain by the bold underline. Only the central region of F10E9.6 exhibiting homology with the Grb7 family is shown. Amino acid residues for each protein are
       numbered (from the initiation methionine) on the right.
L2
      ANSWER 24 OF 156 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 13
ΑN
       10360583 IFIPAT; IFIUDB; IFICDB
TI
       METHODS AND COMPOSITIONS FOR INHIBITING GRB7; ADMINISTERING A
       NON-PHOSPHORYLATED TRIPEPTIDES
       Krag David N; Oligino Lyn; Pero Stephanie C
ΙN
PA
       Unassigned Or Assigned To Individual (68000)
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us 2003105000
                         A1 20030605
      US 2001-13815
US 2000-245755P
                              20011105
PRAI
                              20001103 (Provisional)
      US 2003105000
                              20030605
       Utility; Patent Application - First Publication
       CHEMICAL
       APPLICATION
CLMN
       93
        16 Figure(s).
      FIG. 1 is a histogram showing the binding of Grb7 binding peptides (G7BP)
       to the SH2 domain of human Grb7 by ELISA.
      FIG. 2 is a histogram showing the binding of a control phage clone to the
       SH2 domain of Grb2 but not to the SH2 domain of Grb7.
     FIG. 3 is a histogram showing the effect of mutation on a G7BP-4 phage clone on its ability to bind to the SH2 domain of Grb7.
FIG. 4 is a histogram showing the binding specificity of seven Grb7
       binding peptides to the SH2 domains of Grb7, Grb7 beta D5beta D6,
                       , full length Grb2, and BSA using a phage ELISA.
         ***Grb14***
      FIG. 5A is a graph showing the inhibition of G7-18 peptide-phage binding
     to Grb7-SH2 with the free synthetic peptides G7-18, G718NATE and G7-8. FIG. 5B is a graph showing the inhibition of G7-8NA peptidephage binding
     to Grb7-SH2 with the free synthetic peptides G7-8, G7-8NA and G7-8NATE. FIG. 6A is a graph showing G7-18NATE inhibits the association of Grb7 with the ErbB family of receptors, as detected by antiphosphotyrosine. FIG. 6B is a densitometric analysis of autoradiographs using the Biorad
       Fluor-S Multimager with Quantity One 4.2.1 software, showing G7-18NATE inhibits the association of Grb7, not Grb2, with the ErbB family in a
       dose-dependent manner.
      FIG. 7A is a graph showing that G7-18NATE inhibits the association of Grb7
       with ErbB3 specifically in a dose-dependent manner, as detected by
       anti-ErbB3 FIG. 7B is a densitometric analysis of autoradiographs using
       the Biorad Fluor-S Multimager with Quantity One 4.2.1 software showing
       that G7-18NATE inhibits the association of Grb7 with ErbB3 in a
       dose-dependent manner.
      FIG. 8A is a graph showing that G7-18NATE inhibits the association of Grb7
       with ErbB2 specifically in a dose-dependent manner, as detected by
       anti-ErbB2.
      FIG. 8B is a densitometric analysis of autoradiographs using the Biorad
       Fluor-S Multimager with Quantity One 4.2.1 software showing that
       G7-18NATE inhibits the association of Grb7 with ErbB2 in a dose-dependent
       manner.
      FIG. 9A is one possible chemical structure for G7BP-4NATE (SEQ ID NO:50).
       Other thioether linkages are illustrated in FIGS. 9B, 9C, 9D and 9E, and
       it is to be understood that any of these linkages can be used in the
       formation of G7BP-4NATE.
      FIG. 9B is the structure of a thioether containing peptide (G1TE) . This
       structure illustrates one possible thioether linkage between the N and C
       terminals of a peptide that can be used in the thioether containing
       peptides of the invention.
      FIG. 9C is another possible structure for the thioether containing peptide
       GI TE. This structure illustrates one possible thioether linkage between
       the N and C terminals of a peptide that can be used in the thioether
       containing peptides of the invention.
      FIG. 9D is another possible structure for the thioether containing peptide
       GITE. This structure illustrates one possible thioether linkage between
       the N and C terminals of a peptide that can be used in the thioether containing peptides of the invention.
      FIG. 9E is another possible structure for the thioether containing peptide
       GI TE. This structure illustrates one possible thioether linkage between
       the N and C terminals of a peptide that can be used in the thioether
       containing peptides of the invention.
     ANSWER 25 OF 156 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 14
       10300425 IFIPAT; IFIUDB; IFICDB
       GDU, A NOVEL SIGNALLING PROTEIN; NUCLEOTIDE SEQUENCES CODING POLYPEPTIDE
       FOR USE IN THE DIAGNOSIS, TREATMENT AND PREVENTION OF CANCER
       Daly Roger John (AU); Sutherland Robert Lyndsay (AU)
       Unassigned Or Assigned To Individual (68000)
       US 2003044834 A1 20030306
       US 2002-242332
                              20020911
      WO 1996-AU258
                              19960502 Section 371 PCT Filing UNKNOWN
                             19980422 DIVISION
      US 1998-945771
                                                                   6465623
      AU 1995-2742
PRAI
                              19950502
      US 2003044834
                              20030306
       US 6465623
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Utility: Patent Application - First Publication

PΙ

ΑI

FΙ

DT FS

GI

L2

ΑN

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IN

PA

PΙ ΑI

RLI

FI

DT

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APPLICATION
CLMN
        3 Figure(s).
GΙ
                                                            ***Grb14***
      FIG. 1 shows a schematic representation of
                                                                              structure with
       a restriction map for the ***Grb14***
to derive the ***Grb14*** sequence a
                                                         cDNA and the cDNA clones used
                                           sequence aligned underneath. The initial
       clone isolated by CORT screening was designated clone 1. Two other clones
       (1-1 and 1-2) were isolated from the 184 cell line library by screening
                                             ***Grb14***
       using clone 1 as a probe. The
                                                             cDNA sequence was completed
       using two clones L5 and L6, isolated from a human liver cDNA library.
       Abbreviations are as follows: A; Apa I; Av; Avr II, X; Xho I; E; Eco RI.
       The numbers refer to distance in bp.
      FIG. 2 shows the nucleotide and amino acid sequence of
                                                                           ***Grb14***
       The PH domain is underlined and the SH2 domain indicated by bold type.
       The translation termination codon is shown by an asterisk in the amino
       acid sequence. Numbers refer to distances in bp.
       IG. 3 shows the sequence homology between ***Grb14*** , Grb7, Grb10 and F10E9.6. As alignment of the amino acid sequences of ***Grb14***
                                                            ***Grb14***
      FIG. 3 shows the sequence homology between
       mouse Grb7, mouse Grb10 and C. elegans F10E9.6 was obtained using the
       computer programs Clustal W and SeqVu. Identical residues are boxed. A highly conserved proline-rich motif is indicated by the dotted underline,
       the PH domain by the broken underline and the SH2 domain by the bold underline. Only the central region of F10E9.6 exhibiting homology with the Grb7 family is shown. Amino acid residues for each protein are
       numbered (from the initiation methionine) on the right.
L2
      ANSWER 26 OF 156 USPATFULL ON STN
        2003:330145 USPATFULL
ΑN
        Skin cell biomarkers and methods for identifying biomarkers using
ΤI
        nucleic acid microarrays
IN
        Dooley, Thomas P., Vestavia Hills, AL, UNITED STATES
        Curto, Ernest V., Huntsville, AL, UNITED STATES
        Davis, Richard L., JR., Homewood, AL, UNITED STATES US 2003232356 A1 20031218 US 2003-361006 A1 20030210 (10)
PΙ
ΑI
        US 2002-354519P
                                20020208 (60)
PRAI
        Utility
DT
FS
        APPLICATION
LN.CNT 1897
        INCLM: 435/006.000
INCL
        INCLS: 702/020.000
NCL
        NCLM: 435/006.000
        NCLS:
                702/020.000
IC
         [7]
        ICM: C12Q001-68
        ICS: G06F019-00; G01N033-48; G01N033-50
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
L2
      ANSWER 27 OF 156 USPATFULL ON STN
        2003:225702 USPATFULL
ΑN
        Polynucleotide encoding a novel pleckstrin homology domain and proline
TI
        rich domain containing adapter protein, PMN29
        Finger, Joshua N., San Marcos, CA, UNITED STATES
Perez-Villar, Juan J., Mercerville, NJ, UNITED STATES
ΙN
        Rajashekar, Reddy, Langhorne, PA, UNITED STATES
Yang, Guchen, Morrisville, PA, UNITED STATES
Kiener, Peter A., Doylestown, PA, UNITED STATES
        US 2003157514
                                     20030821
PΙ
                               Αĺ
        US 2002-234816
                                      20020904 (10)
ΑI
                               Α1
PRAI
        US 2001-317063P
                                20010904 (60)
        Utility
DT
        APPLICATION
FS
LN.CNT 13865
INCL
        INCLM: 435/006.000
        INCLS: 435/069.100; 435/320.100; 435/325.000; 530/350.000; 536/023.500;
                 435/007.200
NCL
        NCLM:
                 435/006.000
        NCLS:
                 435/069.100; 435/320.100; 435/325.000; 530/350.000; 536/023.500;
                 435/007.200
IC
        [7]
        ICM: C12Q001-68
        ICS: G01N033-53; G01N033-567; C07H021-04; C12P021-02; C12N005-06;
        C07K014-47
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CAS INDEXING IS AVAILABLE FOR THIS PATENT.

FS

CHEMICAL

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L2
     ANSWER 28 OF 156 USPATFULL ON STN
       2003:37578 USPATFULL
ΑN
TI
       Specimen-linked G protein coupled receptor database
       Muraca, Patrick J., Pittsfield, MA, UNITED STATES
IN
PΙ
       us 2003027223
                           Α1
                                20030206
       US 2002-184694
                                20020628 (10)
ΑI
                           Α1
PRAI
       US 2001-302316P
                            20010629 (60)
       Utility
DT
FS
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LN.CNT 3618
INCL
       INCLM: 435/007.210
       INCLS: 702/019.000
              435/007.210
NCL
       NCLM:
       NCLS:
              702/019.000
       [7]
IC
       ICM: G01N033-567
       ICS: G06F019-00; G01N033-48; G01N033-50
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
L2
     ANSWER 29 OF 156 USPATFULL on STN
       2003:222015 USPATFULL
ΑN
       Compositions for the detection of blood cell and immunological response
TT
       gene expression
       Cocks, Benjamin G., Sunnyvale, CA, United States
IN
       Stuart, Susan G., Montara, CA, United States
Seilhamer, Jeffrey J., Los Altos Hills, CA, United States
       Incyte Corporation, Palo Alto, CA, United States (U.S. corporation)
PA
                           В1
PΙ
       US 6607879
                                20030819
       us 1998-23655
                                19980209 (9)
ΑI
DT
       Utility
FS
       GRANTED
LN.CNT 3719
INCL
       INCLM: 435/006.000
       INCLS: 435/069.100; 536/023.100; 536/024.100; 536/024.300; 536/024.310;
               536/024.320; 536/024.330
NCL
       NCLM:
              435/006.000
       NCLS:
              435/069.100; 536/023.100; 536/024.100; 536/024.300; 536/024.310;
              536/024.320; 536/024.330
IC
       [7]
       ICM: C12Q001-68
       ICS: C07H021-00
EXF
       435/6; 435/69.1; 536/22.1; 536/23.1; 536/24.1; 536/24.3-24.33
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
     ANSWER 30 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
L2
     DUPLICATE 15
     2003:254017
ΑN
                  BIOSIS
     PREV200300254017
DN
ΤI
     Structural basis for dimerization of the Grb10 Src homology 2 domain.
     Implications for ligand specificity.
     Stein, Evan G.; Ghirlando, Rodolfo; Hubbard, Stevan R. [Reprint Author]
ΑU
CS
     Skirball Institute of Biomolecular Medicine, New York University School of
     Medicine, 540 First Ave., New York, NY, 10016, USA
     hubbard@saturn.med.nyu.edu
     Journal of Biological Chemistry, (April 11 2003) Vol. 278, No. 15, pp.
S0
     13257-13264. print.
     CODEN: JBCHA3. ISSN: 0021-9258.
DT
     Article
     English
LA
FD
     Entered STN: 28 May 2003
     Last Updated on STN: 28 May 2003
L2
     ANSWER 31 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
     DUPLICATE 16
     2003:355616
                  BIOSIS
DN
     PREV200300355616
TI
     NIK is a component of the EGF/heregulin receptor signaling complexes.
ΑU
     Chen, Danying; Xu, Liang-Guo; Chen, Lei; Li, Lixia; Zhai, Zhonghe; Shu,
     Hong-Bing [Reprint Author]
CS
     Department of Immunology, National Jewish Medical and Research Center
     University of Colorado Health Sciences Center, 1400 Jackson Street, K516c,
     Denver, CO, 80206, USA
     shuh@njc.org
     Oncogene, (10 July 2003) Vol. 22, No. 28, pp. 4348-4355. print.
SO
     ISSN: 0950-9232 (ISSN print).
     Article
DT
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English
      Entered STN: 6 Aug 2003
ED
      Last Updated on STN: 6 Aug 2003
      ANSWER 32 OF 156 LIFESCI
                                            COPYRIGHT 2004 CSA on STN
L2
      2003:53872 LIFESCI
ΑN
TI
      The Grb10/Nedd4 Complex Regulates Ligand-Induced Ubiquitination and
      Stability of the Insulin-Like Growth Factor I Receptor
      Vecchione, A.; Marchese, A.; Henry, P.; Rotin, D.; Morrione, A.*
Department of Urology and Kimmel Cancer Center, Thomas Jefferson
ΑU
CS
      University, BLSB Room 631, 233 South 10th St., Philadelphia, PA 19107; E-mail: Andrea.Morrione@mail.tju.edu
      Molecular and Cellular Biology [Mol. Cell. Biol.], (20030500) vol. 23, no.
      9, pp. 3363-3372. ISSN: 0270-7306.
      Journal
DT
FS
      English
LA
SL
      English
        ANSWER 33 OF 156 DRUGU COPYRIGHT 2004 THOMSON DERWENT ON STN
L2
        2004-08282 DRUGU
                                 ΡВ
AN
TI
        Imatinib_induces mitochondria-dependent apoptosis of the Bcr-Abl-positive
        K562 cell line and its differentiation toward the erythroid lineage.
        Jacquel A; Herrant M; Legros L; Belhacene N; Luciano F; Pages G; Hofman
ΑU
        P; Auberger P
        Nice, Fr.
10
        FASEB J. (17, No. 14, 2160-62, 2003) 3 Fig.
S0
        CODEN: FAJOEC
                                 ISSN: 0892-6638
        INSERM U526, Physiopathologie de la Survie et de la Mort Cellulaires et
        Infections Virales Equipe Labellisee par la LNC, 06107 Nice-Cedex 2,
        France. (P.A.). (e-mail: auberger@unice.fr).
LA
        English
        Journal
DT
       AB; LA; CT
FA
FS
        Literature
      ANSWER 34 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
L2
AN
      2003:476188 BIOSIS
DN
      PREV200300476188
      Characterization of a novel gene (HGP1) potentially involved in
TI
      osteosarcoma progression.
      Eppert, Kolja [Reprint Author]; Aneliunas, Vicky [Reprint Author]; Wunder, Jay S. [Reprint Author]; Andrulis, Irene L. [Reprint Author] Fred A. Litwin Centre for Cancer Genetics, Samuel Lunenfeld Research Institute, Mount Sinai Hospital, Toronto, ON, Canada Proceedings of the American Association for Cancer Research Annual Meeting, (July 2003) Vol. 44, pp. 1041-1042. print.

Meeting Info.: 94th Annual Meeting of the American Association for Cancer
ΑU
S0
      Research. Washington, DC, USA. July 11-14, 2003.
      ISSN: 0197-016x.
      Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
DT
      Enalish
ED
      Entered STN: 15 Oct 2003
      Last Updated on STN: 15 Oct 2003
L2
      ANSWER 35 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
      DUPLICATE 17
ΑN
      2004:49749 BIOSIS
DN
      PREV200400053388
TI
      Using gene expression profiling to identify the molecular basis of the
      synergistic actions of hepatocyte growth factor and vascular endothelial
      growth factor in human endothelial cells.
      Gerritsen, Mary E. [Reprint Author]; Tomlinson, James E.; Zlot, Constance; Ziman, Michael; Hwang, Stuart 541 Parrott Drive, San Mateo, CA, 94402, USA
ΑU
CS
      meg570@comcast.net
      British Journal of Pharmacology, (October 2003) Vol. 140, No. 4, pp.
SO
      595-610. print.
      ISSN: 0007-1188 (ISSN print).
DT
      Article
      English
IΑ
ED
      Entered STN: 21 Jan 2004
```

Last Updated on STN: 21 Jan 2004

ANSWER 36 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN L2 DUPLICATE 18 2003:451765 BIOSIS AN PREV200300451765 DN Carcinogen mediated initiation of glial progenitors in the rat brain TI results in marked dependency of proliferation and differentiation by insulin and FGF-2. Kokkinakis, Demetrius Michael [Reprint Author]; Yang, Shuting [Reprint AU Authorl CS University of Pittsburgh, Pittsburgh, PA, USA Proceedings of the American Association for Cancer Research Annual S0 Meeting, (July 2003) Vol. 44, pp. 482. print. Meeting Info.: 94th Annual Meeting of the American Association for Cancer Research. Washington, DC, USA. July 11-14, 2003. ISSN: 0197-016X. Conference; (Meeting)
Conference; Abstract; (Meeting Abstract) DT English Entered STN: 1 Oct 2003 FD Last Updated on STN: 1 Oct 2003 ANSWER 37 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN L2 **DUPLICATE 19** 2003:587917 BIOSIS AN PREV200300570714 DN The PIR domain of ***Grb14*** is an intrinsically unstructured protein: Implication in insulin signaling. Moncoq, Karine; Broutin, Isabelle [Reprint Author]; Larue, Valery; Perdereau, Dominique; Cailliau, Katia; Browaeys-Poly, Edith; Burnol, Anne-Francoise; Ducruix, Arnaud Laboratoire de Cristallographie et RMN Biologiques, Faculte de Pharmacie Paris 5, 4 avenue de l'Observatoire, 75270, Paris Cedex, 06, France broutin@pharmacie.univ-paris5.fr FEBS Letters, (20 November 2003) Vol. 554, No. 3, pp. 240-246. print. SO CODEN: FEBLAL. ISSN: 0014-5793. Article English Entered STN: 10 Dec 2003 ED Last Updated on STN: 10 Dec 2003 ANSWER 38 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN L2 DUPLICATE 20 ΑN 2003:390017 BIOSIS PREV200300390017 DN Inhibition of FGF receptor signalling in Xenopus oocytes: Differential TT ***Grb14*** effect of Grb7, Grb10 and Cailliau, Katia; Le Marcis, Veronique; Bereziat, Veronique; Perdereau, Dominique; Cariou, Bertrand; Vilain, Jean Pierre; Burnol, Anne-Francoise; AU Browaeys-Poly, Edith [Reprint Author] Laboratoire de Biologie du Developpement, Universite des Sciences; CS Technologies de Lille, UPRES UA 1033, IFR 118, Batiment SN3, Villeneuve d'Ascq Cedex, France edith.browaeys@univ-lille1.fr FEBS Letters, (31 July 2003) Vol. 548, No. 1-3, pp. 43-48. print. CODEN: FEBLAL. ISSN: 0014-5793. SO Article English LA Entered STN: 27 Aug 2003 ED Last Updated on STN: 27 Aug 2003 L2 ANSWER 39 OF 156 DISSABS COPYRIGHT (C) 2004 ProQuest Information and Learning Company: All Rights Reserved on STN Order Number: AAIMQ78889 ΑN 2004:5360 DISSABS Mitochondrial membrane binding and protein complexing of the ΤI anti-apoptotic adaptor protein Grb10 Hassard, Jennifer L. [M.Sc.]; Thomas, David [advisor] AU McGill University (Canada) (0781) Masters Abstracts International, (2002) Vol. 41, No. 6, p. 1674. Order No.: AAIMQ78889. 75 pages. CS SO ISBN: 0-612-78889-X. DT Dissertation FS MAI English LA ED Entered STN: 20040107 Last Updated on STN: 20040107

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ANSWER 40 OF 156 CAPLUS COPYRIGHT 2004 ACS ON STN DUPLICATE 21
L2
     2002:285562 CAPLUS
AN
DN
     137:61578
     Expressed gene sets as markers for specific tumors
TI
     Ramaswamy, Sridhar; Golub, Todd B.; Tamayo, Pablo; Angelo, Michael
ΙN
     Whitehead Institute for Biomedical Research, USA; Dana-Farber Cancer
PA
     Institute, Inc.
S0
     PCT Int. Appl., 715 pp.
     CODEN: PIXXD2
DT
     Patent
     English
LA
FAN.CNT 4
                        KIND
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                                                                   DATE
     PATENT NO.
     wo 2002024956
                         A2
                               20020328
                                                wo 2001-xB29287
                                                                   20010919
PΙ
              AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM,
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              RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ,
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     wo 2002024956
                               20030306
     wo 2002024956
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     wo 2002024956
                         Α3
                               20030626
              AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
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              LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL,
              PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG,
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PRAI US 2000-233534P
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                         Ρ
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     wo 2001-US29287
                               20010919
                          W
L2
     ANSWER 41 OF 156 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 22
ΑN
                 IFIPAT;IFIUDB;IFICDB
       GDU, A NOVEL SIGNALLING PROTEIN; IT MAY PROVIDE A TARGET IN DISEASES OR
TI
       CONDITIONS IN WHICH PLATELET DERIVED GROWTH FACTOR RECEPTOR (PDGFR) PLAYS
       A REGULATORY ROLE E.G. WOUND HEALING, FIBROTIC CONDITIONS,
       ATHEROSCLEROSIS
       DALY ROGER JOHN (AU); SUTHERLAND ROBERT LINDSAY (AU)
ΙN
       Unassigned Or Assigned To Individual (68000)
PA
PPA
       Garvan Institute of Medical Research AU (Probable)
PΙ
       us 2002086328
                        A1 20020704
       US 1998-945771
                             19980422
ΑI
       wo 1996-us258
                             19960502
       us 2002086328
                             20020704
FΙ
       us 6465623
                             20021015
       Utility; Patent Application - First Publication
DT
FS
       CHEMICAL
       APPLICATION
CLMN
GΙ
        3 Figure(s).
                                                        ***Grb14***
      FIG. 1 shows a schematic representation of
                                                                        structure with
                                    ***Grb14***
       a restriction map for the
                                                     cDNA and the cDNA clones used
                         ***Grb14*** sequence aligned underneath. The initial
       to derive the
       clone isolated by CORT screening was designated clone 1. Two other clones (1-1 and 1-2) were isolated from the 184 cell line library by screening
       using clone 1 as a probe. The _ ***Grb14***
                                                         cDNA sequence was completed
       using two clones L5 and L6, isolated from a human liver cDNA library.
       Abbreviations are as follows: A; Apa I; Av; Avr II, X; Xho I; E; Eco RI.
       The numbers refer to distance in bp.
                                                                      ***Grb14***
      FIG. 2 shows the nucleotide and amino acid sequence of
       The PH domain is underlined and the SH2 domain indicated by bold type.
       The translation termination codon is shown by an asterisk in the amino
       acid sequence. Numbers refer to distances in bp.
      and F10E9.6. As alignment of the amino acid sequences of ***Grb14***
      FIG. 3 shows the sequence homology between
       mouse Grb7, mouse Grb10 and C. elegans F10E9.6 was obtained using the
       computer programs Clustal W and SeqVu. Identical residues are boxed. A
```

highly conserved proline-rich motif is indicated by the dotted underline, the PH domain by the broken underline and the SH2 domain by the bold underline. Only the central region of F10E9.6 exhibiting homology with the Grb7 family is shown. Amino acid residues for each protein are numbered (from the initiation methionine) on the right.

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L2
     ANSWER 42 OF 156 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 23
       10094016 IFIPAT; IFIUDB; IFICDB
AN
TI
       POTENTIAL EFFECTOR FOR THE GRB7 FAMILY OF SIGNALLING PROTEINS; NUCLEOTIDE
       SEQUENCES CODING SIGNAL TRANSDUCTION PLYPEPTIDE; FOR USE IN THE DIAGNOSIS
       AND TREATMENT OF CANCERS
       DALY ROGER JOHN (AU); SUTHERLAND ROBERT L (AU)
ΙN
       Unassigned Or Assigned To Individual (68000)
PA
PΙ
       US 2002037582
                         Α1
                             20020328
ΑI
          2000-509196
                              20000323
       wo 1998-AU795
                              19980923
      AU 1997-9388
PRAI
                              19970923
                              20020328
       us 2002037582
FI
       Utility; Patent Application - First Publication
DT
FS
       CHEMICAL
       APPLICATION
CLMN
       15
        2 Figure(s).
GΙ
      FIG. 1 provides the nucleotide and amino acid (single letter code)
       sequence of 2.2412. Numbers refer to distances in base pairs.
       Ankyrin-type repeat sequences are underlined. An additional repeat
       sequence is indicated by italics. The stop codon is represented by all asterisk. The original cDNA clone 2. 2412 isolated by the two hybrid
       screen spans nucleotides 6942664 of this sequence.
                                                                       ***Grb14***
      FIG. 2 provides a map of the 2.2412-binding region on
       Structure of the deletion constructs used in the analysis. Ga14 DNA-BD
                                                      ***Grb14***
       fusion constructs encoding full length
                                                                        (FL), the
       Nterminal (N), central region (C) and N-terminal+central region (N+C) were generated in the vector pAS2.1. B. Results of betagalactosidase
       activity assays following transformation of the above plasmids into yeast
       strain Y190 together with the original 2.2412 cDNA clone in pACT-2.
      ANSWER 43 OF 156 CAPLUS COPYRIGHT 2004 ACS on STN
L2
      2002:10730 CAPLUS
AN
DN
      136:49326
      Diagnosis of diseases associated with the immune system using oligomer
      probes to detect cytosine methylation state
      Olek, Alexander; Piepenbrock, Christian; Berlin, Kurt
IN
PA
      Epigenomics A.-G., Germany
SO
      PCT Int. Appl., 32 pp.
      CODEN: PIXXD2
DT
      Patent
LA
      German
FAN.CNT 68
      PATENT NO.
                          KIND DATE
                                                  APPLICATION NO.
                                                                      DATE
PΙ
      wo 2002000928
                          A2
                                 20020103
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      EP 1274865
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                                                  EP 2001-953936
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              AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR 2531589 T2 20031028 JP 2001-575634 20010406
      JP 2003531589
                                                  EP 2001-955278
                                 20031112
      EP 1360319
                                                                      20010406
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AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,

IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

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     us 2004023279
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                             20000630
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                        W
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     WO 2001-EP4016
                        W
                             20010406
     EP 2001-967115
                             20010702
                        Α
                              20010702
     WO 2001-EP7537
                        W
     EP 2002-90203
                             20020605
                        Α
L2
     ANSWER 44 OF 156
                       USPATFULL on STN
       2002:315083 USPATFULL
ΑN
       Nucleic acid sequences associated with baldness
TI
       Pritchard, David, Seattle, WA, UNITED STATES
IN
       Burmer, Glenna, Seattle, WA, UNITED STATES
       Brown, Joseph, Seattle, WA, UNITED STATES
Demas, Vasiliki, Seattle, WA, UNITED STATES
US 2002177566 A1 20021128
PΙ
       us 2001-825096
                                 20010402 (9)
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PRAI
       US 2000-199745P
                            20000425 (60)
       Utility
DT
FS
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LN.CNT 3768
INCL
       INCLM: 514/044.000
       INCLS: 435/006.000; 435/007.210; 424/070.100
               514/044.000
NCL
       NCLM:
       NCLS:
               435/006.000; 435/007.210; 424/070.100
TC
       [7]
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       ICS: C12Q001-68; G01N033-567; A61K007-06
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
L2
     ANSWER 45 OF 156 USPATFULL ON STN
       2002:181561 USPATFULL
ΑN
TI
       Process for in vitro selection of high methol producing genotypes
       Khanuja, Suman Preet Singh, Lucknow, INDIA
IN
       Shasany, Ajit Kumar, Lucknow, INDIA
       Dhawan, Sunita, Lucknow, INDIA
       Darokar, Mahendra Pandurang, Lucknow, INDIA
       Kumar, Tiruppadiripuliyur Ranganathan Santha, Lucknow, INDIA
       Saikia, Dharmendra, Lucknow, INDIA
       Naqui, Arif Ali, Lucknow, INDIA
       Kumar, Sushil, Lucknow, INDIA
       Council of Scientific&Industrial Reaearch, New Delhi, INDIA (non-U.S.
PA
       corporation)
PΤ
       US 6423541
                           в1
                                 20020723
ΑI
       us 2000-531768
                                 20000321 (9)
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DT
FS
       GRANTED
LN.CNT 741
INCL
       INCLM: 435/420.000
       INCLS: 435/410.000; 435/421.000; 435/430.000; 435/430.100; 435/431.000
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              435/420.000
              435/410.000; 435/421.000; 435/430.000; 435/430.100; 435/431.000
       NCLS:
TC
       [7]
       ICM: C12N005-00
EXF
       435/410; 435/420; 435/421; 435/430; 435/430.1; 435/431
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
L2
                        WPIDS COPYRIGHT 2004 THOMSON DERWENT ON STN
     ANSWER 46 OF 156
     2002-547451 [58]
ΑN
                         WPIDS
     C2002-155181
DNC
     Treatment or prophylaxis of a subject having a disorder characterized by
TI
     abnormal interaction of Grb7 and a Grb7 ligand, involves administering to
     a non-phosphorylated peptide to a subject in need of the treatment.
     B04 D16
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DC

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TN
     KRAG, D N; OLIGINO, L; PERO, S C
     (UYVE-N) UNIV VERMONT & STATE AGRIC COLLEGE; (KRAG-I) KRAG D N; (OLIG-I)
     OLIGINO L; (PERO-I) PERO S C
CYC
     23
                     A2 20020510 (200258)* EN
PΙ
     wo 2002036142
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                                                        A61K038-00
        RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR
         W: AU CA JP
     AU 2002020265
                        20020515 (200258)
                                                        A61K038-00
                     A1 20030605 (200339)
     us 2003105000
                                                        A61K038-17
     wo 2002036142 A2 wo 2001-US47400 20011105; AU 2002020265 A AU 2002-20265
ADT
     20011105; US 2003105000 A1 Provisional US 2000-245755P 20001103, US
     2001-13815 20011105
FDT
     AU 2002020265 A Based on WO 2002036142
PRAI US 2000-245755P
                           20001103; US 2001-13815
                                                           20011105
     ICM A61K038-00; A61K038-17
IC
     ANSWER 47 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
L2
     DUPLICATE 24
     2002:492206
                  BIOSIS
AN
DN
     PREV200200492206
     Association of Grb7 with phosphoinositides and its role in the regulation
TI
     of cell migration.
     Shen, Tang-Long; Han, Dong Cho; Guan, Jun-Lin [Reprint author]
ΑU
     Department of Molecular Medicine, Cornell University, Ithaca, NY, 14853,
     USA
     jg19@cornell.edu
     Journal of Biological Chemistry, (August 9, 2002) Vol. 277, No. 32, pp.
SO
     29069-29077. print.
     CODEN: JBCHA3. ISSN: 0021-9258.
DT
     Article
     English
LA
     Entered STN: 18 Sep 2002
FD
     Last Updated on STN: 18 Sep 2002
     ANSWER 48 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
L2
     DUPLICATE 25
     2002:292126
                  BIOSIS
     PREV200200292126
DN
     Identification of novel non-phosphorylated ligands, which bind selectively
TT
     to the SH2 domain of Grb7.
     Pero, Stephanie C.; Oligino, Lyn; Daly, Roger J.; Soden, Amy L.; Liu,
     Chen; Roller, Peter P.; Li, Peng; Krag, David N. [Reprint author]
Department of Surgery, University of Vermont School of Medicine, Given
CS
     Medical Building, Rm. E309, Burlington, VT, 05405, USA
     David.Krag@uvm.edu
     Journal of Biological Chemistry, (April 5, 2002) Vol. 277, No. 14, pp.
SO
     11918-11926. print.
     CODEN: JBCHA3. ISSN: 0021-9258.
     Article
DT
     Enalish
LA
ED
     Entered STN: 15 May 2002
     Last Updated on STN: 15 May 2002
     ANSWER 49 OF 156 CAPLUS COPYRIGHT 2004 ACS ON STN
12
     2002:875636 CAPLUS
DN
     138:151170
     Comparative analysis of mutation frequency of coding and non coding short
ΤI
     mononucleotide repeats in mismatch repair deficient colorectal cancers
     Duval, Alex; Reperant, Maryline; Hamelin, Richard
     INSERM U434, CEPH, Paris, Fr.
CS
S0
     Oncogene (2002), 21(52), 8062-8066
     CODEN: ONCNES; ISSN: 0950-9232
PΒ
     Nature Publishing Group
DT
     Journal
     English
LA
              THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE.CNT
        17
              ALL CITATIONS AVAILABLE IN THE RE FORMAT
     ANSWER 50 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
L2
     DUPLICATE 26
     2002:529717
                  BIOSIS
     PREV200200529717
DN
                                                     and regulates its inhibitory
     The adapter protein ZIP binds
                                      ***Grb14***
TI
     action on insulin signaling by recruiting protein kinase Czeta.
     Cariou, Bertrand; Perdereau, Dominique; Cailliau, Katia; Browaeys-Poly,
ΑU
```

Edith; Bereziat, Veronique; Vasseur-Cognet, Mireille; Girard, Jean;

Burnol, Anne-Francoise [Reprint author] Departement d'Endocrinologie, Institut Cochin, CNRS-INSERM-Universite Rene CS Descartes, 24 Rue du Faubourg Saint-Jacques, 75674, Paris, France burnol@cochin.inserm.fr Molecular and Cellular Biology, (October, 2002) Vol. 22, No. 20, pp. SO 6959-6970. print. CODEN: MCEBD4. ISSN: 0270-7306. Article DTLA English Entered STN: 16 Oct 2002 ED Last Updated on STN: 16 Oct 2002 ANSWER 51 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN L2 **DUPLICATE 27** 2002:207358 **BIOSIS** PREV200200207358 DN Inhibition of insulin receptor catalytic activity by the molecular adapter TI ***Grb14*** Bereziat, Veronique; Kasus-Jacobi, Anne; Perdereau, Dominique; Cariou, ΑU Bertrand; Girard, Jean; Burnol, Anne-Francoise [Reprint author] CS Endocrinologie et Metabolisme, CNRS UPR 1524, Institut Cochin de Genetique Moleculaire, 24 rue du Faubourg Saint-Jacques, 75674, Paris Cedex, 14, France burnol@cochin.inserm.fr Journal of Biological Chemistry, (February 15, 2002) Vol. 277, No. 7, pp. S0 4845-4852. print. CODEN: JBCHA3. ISSN: 0021-9258. DT Article English LA ED Entered STN: 20 Mar 2002 Last Updated on STN: 20 Mar 2002 ANSWER 52 OF 156 CAPLUS COPYRIGHT 2004 ACS on STN L2 2003:3572 CAPLUS ΑN 138:382650 DN Ontogeny and the possible function of a novel epidermal growth factor-like repeat domain-containing protein, NELL2, in the rat brain Kim, Hyun; Ha, Chang Man; Choi, Jungil; Choi, Eun Jung; Jeon, Jongrye; Kim, Changmee; Park, Sang Kyu; Kang, Sang Soo; Kim, Kyungjin; Lee, Byung CS Department of Anatomy, Brain Korea 21 Biomedical Sciences, Korea University College of Medicine, Seoul, S. Korea Journal of Neurochemistry (2002), 83(6), 1389-1400 SO CODEN: JONRA9; ISSN: 0022-3042 PB Blackwell Science Ltd. DT Journal English LA 46 RE.CNT THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT L2 ANSWER 53 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN 2002:396091 BIOSIS AN DN PREV200200396091 TI Gene expression profiling of endometrial carcinomas: Identification of molecular biomarkers. Yap, Oi Wah Stephanie [Reprint author]; Zhu, Shirley [Reprint author]; van de Rijn, Matt [Reprint author]; Longacre, Teri [Reprint author]; Teng, Nelson [Reprint author]; Husain, Amreen [Reprint author] Stanford University Medical Center, Stanford, CA, USA CS Proceedings of the American Association for Cancer Research Annual **SO** Meeting, (March, 2002) Vol. 43, pp. 746. print. Meeting Info.: 93rd Annual Meeting of the American Association for Cancer Research. San Francisco, California, USA. April 06-10, 2002. ISSN: 0197-016x. Conference; (Meeting)
Conference; Abstract; (Meeting Abstract) DT English Entered STN: 24 Jul 2002 ED Last Updated on STN: 24 Jul 2002 L2 ANSWER 54 OF 156 SCISEARCH COPYRIGHT 2004 THOMSON ISI ON STN 2002:207936 SCISEARCH AN GA The Genuine Article (R) Number: 524UV TI Comparison of gene expression in old versus young rat hippocampus by cDNA array

Cho K S; Choi J G; Ha C M; Son Y J; Choi W S; Lee B J (Reprint)

ΑU

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Univ Ulsan, Dept Biol Sci, Ulsan 680749, South Korea (Reprint); Gyeongsang
CS
     Natl Univ, Coll Med, Dept Anat, Chinju 660280, South Korea
CYA
     South Korea
     NEUROREPORT, (4 MAR 2002) Vol. 13, No. 3, pp. 285-289.
SO
     Publisher: LIPPINCOTT WILLIAMS & WILKINS, 530 WALNUT ST, PHILADELPHIA, PA
     19106-3621 USA.
     ISSN: 0959-4965
DT
     Article; Journal
     English
LA
REC
     Reference Count: 26
     *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
L2
     ANSWER 55 OF 156 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
     DUPLICATE 28
ΑN
     2003:124261 BIOSIS
DN
     PREV200300124261
     Assignment of backbone 1H, 13C, and 15N resonances of the SH2 domain of
TI
             ***Grb14***
ΑU
     Scharf, Paul J.; Lyons, Barbara A. [Reprint Author]
     Department of Biochemistry, College of Medicine, University of Vermont,
CS
     Burlington, VT, 05405, USA
     blyons@zoo.uvm.edu
     Journal of Biomolecular NMR, (November 2002) Vol. 24, No. 3, pp. 275-276.
SO
     print.
     issn: 0925-2738 (Issn print).
     Article
DT
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LA
ED
     Entered STN: 5 Mar 2003
     Last Updated on STN: 5 Mar 2003
12
     ANSWER 56 OF 156 SCISEARCH COPYRIGHT 2004 THOMSON ISI ON STN
     2002:524711 SCISEARCH
     The Genuine Article (R) Number: 557XP
GΑ
                                                       ***Grb14***
     The atypical PKC-Interacting protein ZIP binds
     potentiates its inhibitory action on insulin signaling
ΑU
     Cariou B (Reprint); Perdereau D; Cailliau K; Browaeys-Poly E; Bereziat V;
     Girard J; Burnol A F
     DIABETES, (JUN 2002) Vol. 51, Supp. [2], pp. A56-A56. MA 228.
S0
     Publisher: AMER DIABETES ASSOC, 1660 DUKE ST. ALEXANDRIA. VA 22314 USA.
     ISSN: 0012-1797.
DT
     Conference; Journal
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     English
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12
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ΑN
DN
     PREV200300155451
ΤI
     Proteomic Study on the Retinas of RD, RDS and C3B Mice as Well as
     Reconfirming of the Differentially Expressed Proteins by Using RT-PCT.
AU
     Li, D. [Reprint Author]; Zhang, Q. J.
     Ocular Genetics and Molec Bio, Zhonghsan Ophthalmic Ctr, GuanZhou, China
CS
     ARVO Annual Meeting Abstract Search and Program Planner, (2002) vol. 2002,
     pp. Abstract No. 3629. cd-rom.
     Meeting Info.: Annual Meeting of the Association For Research in Vision
     and Ophthalmology. Fort Lauderdale, Florida, USA. May 05-10, 2002.
DT
     Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
     English
ED
     Entered STN: 26 Mar 2003
     Last Updated on STN: 26 Mar 2003
12
     ANSWER 58 OF 156 CAPLUS COPYRIGHT 2004 ACS ON STN
     2001:798473
AN
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     135:340282
DN
    Nucleic acid sequences associated with baldness and uses in detecting the
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      New York University School of Medicine, 540 First Avenue, New York, NY,
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     binding protein hGrb10gamma.
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     Antonio, TX 78284-7764, USA
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     DUPLICATE 44
     1997:221295 BIOSIS
     PREV199799513011
DN
     Structural determinants of the interaction between the erbB2 receptor and
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     the Src homology 2 domain of Grb7.
     Janes, Peter W.; Lackmann, Martin; Church, W. Bret; Sanderson, Georgina
     M.; Sutherland, Robert L.; Daly, Roger J. [Reprint author]
     Cancer Res. Program, Garvan Inst. Med. Res., St. Vincent's Hosp., Sydney,
CS
     NSW 2010, Australia
     Journal of Biological Chemistry, (1997) Vol. 272, No. 13, pp. 8490-8497.
SO
     CODEN: JBCHA3. ISSN: 0021-9258.
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     Last Updated on STN: 22 May 1997
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     Human GRB-IR-beta/GRB10: Splice variants of an insulin and growth factor
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     receptor-binding protein with PH and SH2 domains.
     Frantz, J. Daniel; Giorgetti-Peraldi, Sophie; Ottinger, Elizabeth A.;
ΑU
     Shoelson, Steven E. [Reprint author]
     Joslin Diabetes Cent., One Joslin Place, Boston, MA 02215, USA
Journal of Biological Chemistry, (1997) Vol. 272, No. 5, pp. 2659-2667.
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DT
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     Last Updated on STN: 10 Mar 1997
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     126:43162
     GDU: a new target for the erbB family of protein tyrosine kinases and a
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     cDNA encoding it
IN
     Daly, Roger John; Sutherland, Robert Lyndsay
     Garvan Institute of Medical Research, Australia; Daly, Roger John;
PA
     Sutherland, Robert Lyndsay
SO
     PCT Int. Appl., 15 pp.
     CODEN: PIXXD2
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     Cloning and characterization of
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     GRB7 gene family.
     Daly, Roger J. [Reprint author]; Sanderson, Georgina M.; Janes, Peter W.;
AU
     Sutherland, Robert L.
     Cancer Biol. Div., Garvan Inst. Med. Res., St. Vincent's Hosp., Sydney,
     NSW 2010, Australia
Journal of Biological Chemistry, (1996) Vol. 271, No. 21, pp. 12502-12510.
SO
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Entered STN: 24 Oct 1996
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     Assignment of the human
     fluorescence in situ hybridization.
     Baker, Elizabeth; Sutherland, Grant R.; Sutherland, Robert L.; Daly, Roger
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     Cancer Biol. Div., Garvan Inst. Med. Res., St. Vincent's Hosp., Sydney,
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     Genomics, (1996) Vol. 36, No. 1, pp. 218-220.
     CODEN: GNMCEP. ISSN: 0888-7543.
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      Identification and selection of specific interaction agents by phage
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      display, comprises using a carrier with a polymer-free surface to which affinity ligands are bound.
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      Daly R J; Sutherland R L
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DATE (DATE):
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     These sequences were made by sequencing genomic exons and ordering
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                        Kejariwal, A.; Todd, M.A.; Tanenbaum, D.M.; Civello, D.R.;
                         Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
                        White, T.J.; Sninsky, J.J.; Adams, M.D.; Cargill, M.
                         Inferring nonneutral evolution from human-chimp-mouse
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                        orthologous gene trios
                        science, 302 (5652), 1960-1963 (2003)
   JOURNAL (SO):
   OTHER SOURCE (OS):
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Inferring nonneutral evolution from human-chimp-mouse
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   TITLE (TI):
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Science, 302 (5652), 1960-1963 (2003)
CA 140:140421
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   AUTHOR (AU):
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COMMENT:
     These sequences were made by sequencing genomic exons and ordering
     them based on alignment.
REFERENCE:
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                         Clark, A.G.; Glanowski, S.; Nielson, R.; Thomas, P.;
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                         Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
                         White, T.J.; Sninsky, J.J.; Adams, M.D.; Cargill, M. Inferring nonneutral evolution from human-chimp-mouse
   TITLE (TI):
                         orthologous gene trios
Science, 302 (5652), 1960-1963 (2003)
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                         Lu,F.; Murphy,B.; Ferriera,S.; Wang,G.; Zheng,X.H.;
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LOCUS (LOC):
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DATE (DATE)
                        30 Jun 2004
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COMMENT:
     Contact: MGC help desk
     Email: cgapbs-r@mail.nih.gov
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     CDNA Library Preparation: Life Technologies, Inc.
     CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
     DNA Sequencing by: National Institutes of Health Intramural
     Sequencing Center (NISC),
     Gaithersburg, Maryland;
     Web site: http://www.nisc.nih.gov/
     Contact: nisc_mgc@nhgri.nih.gov
     Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

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                               Strausberg, R.L.; Feingold, E.A.; Grouse, L.H.;
Derge, J.G.; Klausner, R.D.; Collins, F.S.; Wagner, L.;
Shenmen, C.M.; Schuler, G.D.; Altschul, S.F.; Zeeberg, B.;
   AUTHOR (AU):
                               Buetow, K.H.; Schaefer, C.F.; Bhat, N.K.; Hopkins, R.F.;
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                               Generation and initial analysis of more than 15,000
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                               Direct Submission
    TITLE (TI):
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                               Submitted (09-JUN-2003) National Institutes of Health,
                               Mammalian Gene Collection (MGC), Cancer Genomics
                               Office, National Cancer Institute, 31 Center Drive,
                               Room 11A03, Bethesda, MD 20892-2590, USA
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DATE (DATE):
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       Economy, Trade and Industry of Japan; cDNA full insert sequencing:
       Research Association for Biotechnology; cDNA library construction:
       Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported
       by Japan Key Technology Center etc.).
REFERENCE:
   AUTHOR (AU):
                                  Isogai,T.; Ota,T.; Nishikawa,T.; Hayashi,K.; Otsuki,T.;
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JOURNAL (SO):

Unpublished

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   AUTHOR (AU):
                            Isogai,T.; Otsuki,T.
   TITLE (TI):
                            Direct Submission
                             Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu,
   JOURNAL (SO):
                             Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp,
                            Tel:81-438-52-3975, Fax:81-438-52-3986)
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DATE (DATE):
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COMMENT:
      Contact: MGC help desk
      Email: cgapbs-r@mail.nih.gov
      Tissue Procurement: Gilbert Smith, Ph.D.
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      Sequencing Center
      Center code: BCM-HGSC
      Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Contact: amg@bcm.tmc.edu
       Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
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    TITLE (TI):
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    TITLE (TI):
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    JOURNAL (SO):
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                                GENBANK.RTM. COPYRIGHT 2004 on STN
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Identification of a novel human tankyrase through its
    AUTHOR (AU):
   TITLE (TI):
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    TITLE (TI):
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    JOURNAL (SO):
                              Institute of Medical Research, 384 Victoria St.,
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COMMENT:
       Contact: Yoshihide Hayashizaki
       Laboratory for Genome Exploration Research Group, RIKEN Genomic
       Sciences Center(GSC), Yokohama Institute
       The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216
       Email: genome-res@gsc.riken.go.jp
       URL:http://genome.gsc.riken.go.jp/
       Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
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       Thermostabilization and thermoactivation of thermolabile enzymes by
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       CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
        Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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        Automated filtration-based high-throughput plasmid preparation
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        Carninci, P. and Hayashizaki, Y.
        High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
       19-44 (1999)
        Please visit our web site (http://genome.rtc.riken.go.jp) for
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REFERENCE:
                                Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.; Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.; Hori, F.; Ishikawa, J.; Ishikawa, T.; Itoh, M.;
    AUTHOR (AU):
                                Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.; Kawai,J.;
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                                           RIKEN. Division of Experimental
                                           Animal Research in Riken
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COMMENT:
     Contact: Yoshihide Hayashizaki
     Laboratory for Genome Exploration Research Group, RIKEN Genomic
```

```
Sciences Center(GSC), Yokohama Institute
       The Institute of Physical and Chemical Research (RIKEN)
       1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
       Fax: 81-45-503-9216
       Email: genome-res@gsc.riken.go.jp,
       URL:http://genome.gsc.riken.go.jp/
       Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
       Thermostabilization and thermoactivation of thermolabile enzymes by
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        Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                          RIKEN. Division of Experimental
Animal Research in Riken
                                                          contributed to prepare mouse
                                                          tissues. 1st strand cDNA was primed with a primer [5'
                                                          GAGAGAGAGAGCGCCGCAACTCGAGTTTTTTTT
                                                          TTTTTTTVN 3'], cDNA was prepared
                                                          by using trehalose
                                                          thermo-activated reverse
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                                                          adapter of sequence [5'
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GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC

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L2
      ANSWER 102 OF 156
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NUCLEIC ACID COUNT (NA): 117 a
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COMMENT:
       Contact: Yoshihide Hayashizaki
       Laboratory for Genome Exploration Research Group, RIKEN Genomic
       Sciences Center(GSC), Yokohama Institute
       The Institute of Physical and Chemical Research (RIKEN)
       1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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      Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
       Thermostabilization and thermoactivation of thermolabile enzymes by
       trehalose and its application for the synthesis of full length
      cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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        Please visit our web site (http://genome.rtc.riken.go.jp) for
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REFERENCE:
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                                 Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.; Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.;
    AUTHOR (AU):
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                                 Shibata, Y.,; Shigemoto, Y.; Shinagawa, A.; Shiraki, T.;
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Tagawa,A.; Takahashi,F.; Tominaga,N.; Toya,T.a;
Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
Yamanaka,I., Yano,R.H; Yasunishi,A.; Yokota,T.;
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   TITLE (TI):
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Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

62 g

62 c

COMMENT:

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Tel: 81-45-503-9222
Fax: 81-45-503-9216
      Email: genome-res@gsc.riken.go.jp,
      URL:http://genome.gsc.riken.go.jp/
      Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
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      Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length
      cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
        Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
      Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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       Automated filtration-based high-throughput plasmid preparation
      system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
      19-44 (1999)
        Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
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                               Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.;
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                               Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.;
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                               Yamanaka, I., Yano, R.H; Yasunishi, A.; Yokota, T.;
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                                                    Genome Science Laboratory in
                                                    RIKEN. Division of Experimental
                                                    Animal Research in Riken
                                                    contributed to prepare mouse
                                                    tissues. 1st strand cDNA was
                                                    primed with a primer [5]
                                                    GAGAGAGAGCGGCCGCAACTCGAGTTTTTTT
                                                    TTTTTTTVN 3'], cDNA was prepared
                                                    by using trehalose
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with BamHI and XhoI. Vector: a

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    301 gttaaaatta aaccttatt
      ANSWER 104 OF 156
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DATE (DATE):
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SOURCE:
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Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 74 a 54 c 49 g 73 t
COMMENT:
       Contact: Yoshihide Hayashizaki
       Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
       Fax: 81-45-503-9216
       Email: genome-res@gsc.riken.go.jp,
       URL:http://genome.gsc.riken.go.jp/
      Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
       Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
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       ,Y. and Hayashizaki,Y.
        Automated filtration-based high-throughput plasmid preparation
       system. Genome Res. 9 (5), 463-470 (1999)
        Carninci, P. and Hayashizaki, Y.
        High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
        Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                1 (bases 1 to 250)
                               Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.; Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.;
    AUTHOR (AU):
                               Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.;
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Tsunoda,Y.; Watahiki,A.; Watanabe,S.; Yamamura,T.;
Yamanaka,I., Yano,R.H; Yasunishi,A.; Yokota,T.;
Yoshida,K.; Yoshiki,A.; Yoshino,M..; Muramatsu,M.;
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    TITLE (TI):
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    JOURNAL (SO):
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                                               Riken Genomic Sciences Center and
                                               Genome Science Laboratory in
                                               RIKEN. Division of Experimental
                                               Animal Research in Riken
                                               contributed to prepare mouse
                                               tissues. 1st strand cDNA was
                                               primed with a primer [5
                                               GAGAGAGAGCGCCCGCAACTCGAGTTTTTTTT
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L2
      ANSWER 105 OF 156
                                               COPYRIGHT 2004 on STN
                               GENBANK.RTM.
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SOURCE:
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Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 106 a
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COMMENT:
      Contact: Yoshihide Hayashizaki
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Laboratory for Genome Exploration Research Group, RIKEN Genomic

The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,

Sciences Center(GSC), Yokohama Institute

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URL:http://genome.gsc.riken.go.jp/
      Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
        Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.
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        Automated filtration-based high-throughput plasmid preparation
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        Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
       19-44 (1999)
        Please visit our web site (http://genome.rtc.riken.go.jp) for
       further details.
REFERENCE:
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   AUTHOR (AU):
                                 Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
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                                house mouse.
SOURCE:
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Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 87 a
                                          45 c
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COMMENT:
       Contact: Yoshihide Hayashizaki
       Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216
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      Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
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                                          enriched for full-length by cap-trapper. cDNA went through one
                                          round of normalization to Rot =
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                                          prepared with the primer adapter
                                          of sequence [5
                                          GAGAGAGATTCTCGAGTTAATTAAATTAATCC
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                                          Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"
  1 cctgttcagc ccaactctgt ctcactccct acactacaga agaagaagga ttcacaggtg
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181 ttcctattac actcatgact ttaaatttat tagttaaaat taaaccttat t
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                       Euteleostomi; Mammalia; Eutheria; Rodentia;
                       Sciurognathi; Muridae; Murinae; Mus
                                          54 g
  Laboratory for Genome Exploration Research Group, RIKEN Genomic
  Sciences Center(GSC), Yokohama Institute
  The Institute of Physical and Chemical Research (RIKEN)
  1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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SEQUENCE (SEQ):

LOCUS (LOC):

DATE (DATE):

SOURCE:

COMMENT:

ANSWER 107 OF 156

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MOLECULE TYPE (CI):

DIVISION CODE (CI):

DEFINITION (DEF):

ORGANISM (ORGN):

GenBank ACC. No. (GBN): BB360354

NUCLEIC ACID COUNT (NA): 103 a

Tel: 81-45-503-9222 Fax: 81-45-503-9216

Contact: Yoshihide Hayashizaki

Email: genome-res@gsc.riken.go.jp,

BB360354

284

279047-92-6

mRNA; linear

12 Jul 2000

house mouse. Mus musculus

53 c

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      Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
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      Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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       Automated filtration-based high-throughput plasmid preparation
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       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
       Please visit our web site (http://genome.rtc.riken.go.jp) for
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REFERENCE:
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Yoshida,K.; Yoshiki,A.; Yoshino,M..; Muramatsu,M.;
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                                                 Genome Science Laboratory in
                                                  RIKEN. Division of Experimental
                                                 Animal Research in Riken
                                                  contributed to prepare mouse
                                                  tissues. 1st strand cDNA was
                                                  primed with a primer [5]
                                                  GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT
                                                  TTTTTTTVN 3'], cDNA was prepared
                                                  by using trehalose
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                                                  enriched for full-length by
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                                                  round of normalization to Rot =
                                                  10.0 and subtraction to Rot =
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CCCCCCCCC 3']. cDNA was cloned
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into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5 end: SalI; 3' end: BamHI"

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                                               COPYRIGHT 2004 on STN
L2
     ANSWER 108 OF 156
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LOCUS (LOC):
GenBank ACC. NO. (GBN): BB359872
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CAS REGISTRY NO. (RN):
SEQUENCE LENGTH (SQL):
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MOLECULE TYPE (CI):
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DIVISION CODE (CI):
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DATE (DATE):
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DEFINITION (DEF):
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                            to AF076619 Rattus norvegicus molecular adapter rGrb14
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SOURCE:
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 ORGANISM (ORGN):
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NUCLEIC ACID COUNT (NA): 92 a
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COMMENT:
      Contact: Yoshihide Hayashizaki
     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
      Tel: 81-45-503-9222
      Fax: 81-45-503-9216
      Email: genome-res@gsc.riken.go.jp,
      URL:http://genome.gsc.riken.go.jp/
      Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
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      Thermostabilization and thermoactivation of thermolabile enzymes by
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       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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       Automated filtration-based high-throughput plasmid preparation
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       Carninci, P. and Hayashizaki, Y.
       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
      19-44 (1999)
       Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
                                (bases 1 to 245)
REFERENCE:
   AUTHOR (AU):
                            Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
                            Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.;
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   TITLE (TI):
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JOURNAL (SO): Unpublished (2000)

FEATURES (FEAT):

Feature Key Location Qualifier

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L2 ANSWER 109 OF 156 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC):

GenBank ACC. NO. (GBN):

GenBank VERSION (VER):

CAS REGISTRY NO. (RN):

SEQUENCE LENGTH (SQL):

MOLECULE TYPE (CI):

MRNA; linear

DIVISION CODE (CI): Expressed sequence tag

DATE (DATE): 11 Jul 2000

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rGrb14 (***Grb14***) mRNA, mRNA sequence house mouse.

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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

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Sciurognathi; Muridae; Murinae; Mus

NUCLEIC ACID COUNT (NA): 89 a 69 c 61 g 92 t

COMMENT:

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Contact: Yoshihide Hayashizaki
           Laboratory for Genome Exploration Research Group, RIKEN Genomic
          Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
           Fax: 81-45-503-9216
           Email: genome-res@gsc.riken.go.jp,
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           Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
           Thermostabilization and thermoactivation of thermolabile enzymes by
           trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
              Automated filtration-based high-throughput plasmid preparation
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              Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
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REFERENCE:
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Animal Research in Riken
                                                                                               contributed to prepare mouse
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                                                                                               GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTT
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SOURCE:
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NUCLEIC ACID COUNT (NA): 162 a
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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
      The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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      Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
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      Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki Y. and Hayashizaki Y.
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   AUTHOR (AU):
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                                                  contributed to prepare mouse
                                                  tissues. 1st strand cDNA was
                                                  primed with a primer [5
                                                  GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTTT
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                                                  20.0 and subtraction to Rot =
                                                  459.0. Second strand cDNA was
                                                  prepared with the primer adapter
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                                                  Lambda FLC I. ~Retina RNA was
                                                  provided by Stefano Gustincich,
                                                  Department of Neurobiology
                                                  Harvard Medical School, 220
                                                  Longwood Ave., Boston, MA02115,
                                                  USA, whose assistance we
                                                  gratefully acknowledge
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                                                  COPYRIGHT 2004 on STN
                                 GENBANK.RTM.
      ANSWER 111 OF 156
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SEQUENCE (SEQ):

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LOCUS (LOC):

SEQUENCE LENGTH (SQL):

MOLECULE TYPE (CI):

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mRNA; linear

source

Feature Key

JOURNAL (SO):

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                              1 Aug 2000
DATE (DATE):
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ORGANISM (ORGN):
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                              Euteleostomi; Mammalia; Euthéria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 92 a
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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
      Fax: 81-45-503-9216
      Email: genome-res@gsc.riken.go.jp,
      URL:http://genome.gsc.riken.go.jp/
      Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
       ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
      Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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        Automated filtration-based high-throughput plasmid preparation
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        High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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        Please visit our web site (http://genome.rtc.riken.go.jp) for
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    AUTHOR (AU):
                               Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
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                                                    and sequenced in Mouse Genome
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                                                    Riken Genomic Sciences Center and
                                                    Genome Science Laboratory in
```

RIKEN. Division of Experimental

Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5 GAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5'GAGAGAGAGATTCTCGAGTTAATTAAATTAA TCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. ~Retina RNA was provided by Stefano Gustincich, Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA02115, USA, whose assistance we gratefully acknowledge

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SOURCE:
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NUCLEIC ACID COUNT (NA): 97 a
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COMMENT:
     Contact: Yoshihide Hayashizaki
     Laboratory for Genome Exploration Research Group, RIKEN Genomic
     Sciences Center(GSC), Yokohama Institute
     The Institute of Physical and Chemical Research (RIKEN)
     1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
     Tel: 81-45-503-9222
     Fax: 81-45-503-9216
     Email: genome-res@gsc.riken.go.jp,
     URL:http://genome.gsc.riken.go.jp/
     Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
     Thermostabilization and thermoactivation of thermolabile enzymes by
     trehalose and its application for the synthesis of full length
     CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
      Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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      Automated filtration-based high-throughput plasmid preparation
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Carninci, P. and Hayashizaki, Y.
       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
      19-44 (1999)
       Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
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REFERENCE:
                            Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.;
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                            Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.;
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                                                RIKEN. Division of Experimental
                                                Animal Research in Riken
                                                contributed to prepare mouse
                                                tissues. 1st strand cDNA was primed with a primer [5'
                                                by using trehalose
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BB187252
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SOURCE:
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NUCLEIC ACID COUNT (NA): 105 a
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COMMENT:
       Contact: Yoshihide Hayashizaki
       Laboratory for Genome Exploration Research Group, RIKEN Genomic
       Sciences Center(GSC), Yokohama Institute
       The Institute of Physical and Chemical Research (RIKEN)
       1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
       Tel: 81-45-503-9222
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       Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
       Thermostabilization and thermoactivation of thermolabile enzymes by
       trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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        Automated filtration-based high-throughput plasmid preparation
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
       19-44 (1999)
         Please visit our web site (http://genome.rtc.riken.go.jp) for
       further details.
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     AUTHOR (AU):
                                 Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.;
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BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5 GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTTT TTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5 GAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. "

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NUCLEIC ACID COUNT (NA): 87 a
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     Contact: Yoshihide Hayashizaki
     Laboratory for Genome Exploration Research Group, RIKEN Genomic
     Sciences Center(GSC), Yokohama Institute
     The Institute of Physical and Chemical Research (RIKEN)
     1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
     Tel: 81-45-503-9222
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     Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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     cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
      Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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      Automated filtration-based high-throughput plasmid preparation
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SEQUENCE (SEQ):

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Carninci, P. and Hayashizaki, Y.
       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
      19-44 (1999)
       Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
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REFERENCE:
   AUTHOR (AU):
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                                                   Genome Science Laboratory in
                                                   RIKEN. Division of Experimental
Animal Research in Riken
                                                   contributed to prepare mouse
                                                   tissues. 1st strand cDNA was
                                                   primed with a primer [5
                                                   GAGAGAGAGAGCTCTTTTTTTT
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L2
      ANSWER 115 OF 156
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вв173204

GenBank (R)

LOCUS (LOC):

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                                 house mouse.
SOURCE:
 ORGANISM (ORGN):
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                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi; Mammalia; Eutheria; Rodentia;
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NUCLEIC ACID COUNT (NA): 98 a
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COMMENT:
       Contact: Yoshihide Hayashizaki
       Laboratory for Genome Exploration Research Group, RIKEN Genomic
       Sciences Center(GSC), Yokohama Institute
       The Institute of Physical and Chemical Research (RIKEN)
       1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
       Tel: 81-45-503-9222
Fax: 81-45-503-9216
       Email: genome-res@gsc.riken.go.jp,
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       Thermostabilization and thermoactivation of thermolabile enzymes by
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       CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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        Automated filtration-based high-throughput plasmid preparation
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REFERENCE:
                                     (bases 1 to 282)
                                 Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
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and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5 GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTT TTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5 GAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I.

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L2
     ANSWER 116 OF 156
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LOCUS (LOC):
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GenBank VERSION (VER):
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DATE (DATE)
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                                                  ) mRNA, mRNA sequence.
SOURCE:
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NUCLEIC ACID COUNT (NA): 79 a
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COMMENT:
     Contact: Yoshihide Hayashizaki
     Laboratory for Genome Exploration Research Group, RIKEN Genomic
     Sciences Center(GSC), Yokohama Institute
     The Institute of Physical and Chemical Research (RIKEN)
     1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
     Tel: 81-45-503-9222
     Fax: 81-45-503-9216
     Email: genome-res@gsc.riken.go.jp,
     URL:http://genome.gsc.riken.go.jp/
     Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
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     Thermostabilization and thermoactivation of thermolabile enzymes by
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      Automated filtration-based high-throughput plasmid preparation
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system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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       Please visit our web site (http://genome.rtc.riken.go.jp) for
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REFERENCE:
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                                                   Genome Science Laboratory in
                                                  RIKEN. Division of Experimental Animal Research in Riken
                                                   contributed to prepare mouse
                                                   tissues. 1st strand cDNA was primed with a primer [5'
                                                   GAGAGAGAAGGATCCAAGAGCTCTTTTTTTT
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                                                   GAGAGAGAGTTCTCGAGTTAATTAAATTAATCC
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      ANSWER 117 OF 156
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LOCUS (LOC):

BB124451

GenBank (R)

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SOURCE:
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NUCLEIC ACID COUNT (NA): 108 a
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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
      The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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      Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
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      Thermostabilization and thermoactivation of thermolabile enzymes by
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Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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        Automated filtration-based high-throughput plasmid preparation
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        Carninci, P. and Hayashizaki, Y.
        High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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        Please visit our web site (http://genome.rtc.riken.go.jp) for
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                               Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.; Arakawa,T.; Carninci,P.; Endo,T.; Fukuda,S.; Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.; Ishikawa,J.; Ishikawa,T.; Itoh,M.;
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SOURCE:
                            house mouse.
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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
     The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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     Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
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       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
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Automated filtration-based high-throughput plasmid preparation

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       Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                 GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTT
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SOURCE:
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NUCLEIC ACID COUNT (NA): 110 a
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       19 - \overline{44} (1999)
         Please visit our web site (http://genome.rtc.riken.go.jp) for
       further details.
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    AUTHOR (AU):
                                   Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
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L2
      ANSWER 120 OF 156
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LOCUS (LOC):
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DATE (DATE):
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SOURCE:
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NUCLEIC ACID COUNT (NA): 102 a
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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
      The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
      Fax: 81-45-503-9216
      Email: genome-res@gsc.riken.go.jp
      URL:http://genome.gsc.riken.go.jp/
      Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
      ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
      Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length
      cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
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       Automated filtration-based high-throughput plasmid preparation
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       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
      19-44 (1999)
       Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
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                                                   RIKEN. Division of Experimental
                                                   Animal Research in Riken
                                                   contributed to prepare mouse
                                                   tissues. 1st strand cDNA was
                                                   primed with a primer [5
                                                   GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTT
TTTTTTTVN 3'], cDNA was prepared
                                                   by using trehalose
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                                                   cap-trapper. cDNA went through one
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ANSWER 121 OF 156
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COMMENT:
           Contact: Yoshihide Hayashizaki
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           1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, J., Tomaru, Y
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                                         RIKEN. Division of Experimental Animal Research in Riken
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                                         GAGAGAGAAGGATCCAAGAGCTCTTTTTTTT
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Vector: a modified pBluescript
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 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 URL:http://genome.gsc.riken.go.jp/
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Tel: 81-45-503-9222 Fax: 81-45-503-9216

Contact: Yoshihide Hayashizaki

Email: genome-res@gsc.riken.go.jp,

BB045416

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BB045416.1

272392-50-4

mRNA; linear

23 Jun 2000

house mouse.

Mus musculus

N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

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Thermostabilization and thermoactivation of thermolabile enzymes by

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trehalose and its application for the synthesis of full length
      cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
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                                                  tissues. 1st strand cDNA was
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                                                  GAGAGAGAAGGATCCAAGAGCTCTTTTTTTT
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                                                  thermo-activated reverse
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     ANSWER 123 OF 156
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DATE (DATE):
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SOURCE:
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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
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The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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      ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
      Thermostabilization and thermoactivation of thermolabile enzymes by
      trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
      Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
      ,Y. and Hayashizaki,Y.
       Automated filtration-based high-throughput plasmid preparation
      system. Genome Res. 9 (5), 463-470 (1999)
       Carninci,P. and Hayashizaki,Y.
       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
       Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                (bases 1 to 289)
   AUTHOR (AU):
                             Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
                             Arakawa,T.; Carninci,P. ; Endo,T.; Fukuda,S.;
                             Fukunishi,Y.; Hara,A.; Hayatsu,N.; Hirozane,T.
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                             Kikuchi,N.; Kiyosawa,H.; Kojima,Y.; Kondo,S.; Koya,S.;
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Shibata,Y.,; Shigemoto,Y.; Shinagawa,A.; Shiraki,T.;
                            Sogabe, Y.; Sugahara, Y., Suzuki, H.; Suzuki, H.; Tagawa, A.; Takahashi, F.; Tominaga, N.; Toya, T.a; Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.; Yamanaka, I., Yano, R.H; Yasunishi, A.; Yokota, T.; Yoshida, K.; Yoshiki, A.; Yoshino, M..; Muramatsu, M.;
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   JOURNAL (SO):
FEATURES (FEAT):
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of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCC CCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5 end: SalI; 3' end: BamHI." SEQUENCE (SEQ): 1 tctaccacta cacacggggt ctttcccccc aaccagcagc attactgtcc taggatcccc 61 gtttacccta actctgtgtc actcgttaca ccacagaaga agaaggatcc aaaggagaat 121 gattagagag agagagaga atcacaaggc tgaatacaaa tcatggtgaa aagaagattt 181 cacctgcggg ttacaaaaaa aaaataggtc acacattgca aattagtgaa aacttggatt 241 cctattacac tcatgacttt aaatttatta gttaaaatta aaccttatt L2 ANSWER 124 OF 156 GENBANK.RTM. COPYRIGHT 2004 on STN LOCUS (LOC): BB037605 GenBank (R) GenBank ACC. NO. (GBN): BB037605 GenBank VERSION (VER): BB037605.1 GI:8443991 CAS REGISTRY NO. (RN): 272314-39-3 SEQUENCE LENGTH (SQL): 237 MOLECULE TYPE (CI): mRNA; linear DIVISION CODE (CI): Expressed sequence tag DATE (DATE): 23 Jun 2000 BB037605 RIKEN full-length enriched, 13 days embryo forelimb Mus musculus cDNA clone 5930428012 3' similar DEFINITION (DEF): to AF076619 Rattus norvegicus molecular adapter rGrb14 ***Grb14***) mRNA, mRNA sequence. SOURCE: house mouse. ORGANISM (ORGN): Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NUCLEIC ACID COUNT (NA): 84 a 50 c 40 g

Laboratory for Genome Exploration Research Group, RIKEN Genomic

COMMENT:

Contact: Yoshihide Hayashizaki

Sciences Center(GSC), Yokohama Institute

```
The Institute of Physical and Chemical Research (RIKEN)
       1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
       Tel: 81-45-503-9222
       Fax: 81-45-503-9216
       Email: genome-res@gsc.riken.go.jp,
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       Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki
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       Thermostabilization and thermoactivation of thermolabile enzymes by
       trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carnici,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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        Automated filtration-based high-throughput plasmid preparation
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        Carninci, P. and Hayashizaki, Y.
        High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
       19-44 (1999)
        Please visit our web site (http://genome.rtc.riken.go.jp) for
       further details.
REFERENCE:
                                     (bases 1 to 237)
                                  Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.; Arakawa, T.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.; Hori, F.; Ishikawa, J.; Ishikawa, T.; Itoh, M.; Izawa, M.; Kadota, K.; Kagawa, I.; Kai, C.; Kawai, J.;
    AUTHOR (AU):
                                  Kikuchi, N.; Kiyosawa, H.; Kojima, Y.; Kondo, S.; Koya, S.;
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    TITLE (TI):
                                  RIKEN Mouse ESTs (Konno.H., et al.)
    JOURNAL (SO):
                                  Unpublished (2000)
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BamHI; cDNA library was prepared
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                                                         Encyclopedia Project of Genome
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                                                         Riken Genomic Sciences Center and
                                                         Genome Science Laboratory in
                                                         RIKEN. Division of Experimental
                                                         Animal Research in Riken
                                                         contributed to prepare mouse
                                                         tissues. 1st strand cDNA was
                                                         primed with a primer [5]
                                                         GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTT
                                                         TTTTTTTVN 3'], cDNA was prepared
                                                         by using trehalose
                                                         thermo-activated reverse
                                                         transcriptase and subsequently
                                                         enriched for full-length by
                                                         cap-trapper. cDNA went through one
                                                         round of normalization to Rot =
                                                         10.0 and subtraction to Rot =
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100.0. Second strand cDNA was

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prepared with the primer adapter
                                              of sequence [5
                                              Vector: a modified pBluescript
                                              KS(+) after bulk excision from
                                              Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
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                                          GenBank (R)
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                               9 a 491 c 492
(bases 1 to 1978)
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                                                        436 t
                           Reilly, J.F.; Mickey, G.; Maher, P.A.
Association of fibroblast growth factor receptor 1 with
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                           the adaptor protein
                           of a new receptor binding partner
                           J. Biol. Chem., 275 (11), 7771-7778 (2000)
                           CA 132:330035
                               (bases 1 to 1978)
                           Reilly, J.F.; Mickey, G.; Maher, P.A.
                           Direct Submission
                           Submitted (01-JUN-1999) Cell Biology, The Scripps
Research Institute, 10550 N. Torrey Pines Rd., CAL-3,
La Jolla, CA 92037, USA
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DATE (DATE):

SOURCE:

REFERENCE:

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source

5'UTR

gene ČDS

L2

ANSWER 125 OF 156

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JOURNAL (SO):

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JOURNAL (SO):

TITLE (TI):

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Location

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mRNA; linear

19 Mar 2000

house mouse.

Mus musculus

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      ANSWER 126 OF 156
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NUCLEIC ACID COUNT (NA): 76 a
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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
      The Institute of Physical and Chemical Research (RIKEN)
```

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki

Transcriptional sequencing: A method for DNA sequencing using RNA

Tel: 81-45-503-9222 Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/

```
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
      Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
       Automated filtration-based high-throughput plasmid preparation
      system. Genome Res. 9 (5), 463-470 (1999)
       Carninci, P. and Hayashizaki, Y.
       High-efficiency full-length cDNA cloning, Methods Enzymol, 303,
      19-44 (1999)
       Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
REFERENCE:
                             1 (bases 1 to 207)
                             Konno,H.; Aizawa,K.; Akahira,S.; Akiyama,J.;
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Hayatsu,N.; Hirozane,T.; Hori,F.; Ishii,Y.;
   AUTHOR (AU):
                             Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.;
Kai,C.?; Kawai,J.; Kikuchi,N.; Kojima,Y.; Koya,S.;
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                                                 RIKEN. Division of Experimental
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                                                 185.0 Second strand cDNA was
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                                                 CCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites.
                                                 Vector: a modified pBluescript
                                                 KS(+) after bulk excision from
                                                 Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"
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      ANSWER 127 OF 156
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DEFINITION (DEF):
                               ĂF076619 Rattus norvegicus molecular adapter rGrb14 (
                                  ***Grb14*** ) mRNA, mRNA sequence.
SOURCE:
                               house mouse.
 ORGANISM (ORGN):
                               Mus musculus
                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                               Euteleostomi; Mammalia; Eutheria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 93 a
                                         32 c
                                                  36 g
COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
      The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
      Tel: 81-45-503-9222
       Fax: 81-45-503-9216
      Email: genome-res@gsc.riken.go.jp,
      URL:http://genome.gsc.riken.go.jp/
      Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
       Transcriptional sequencing: A method for DNA sequencing using RNA
      polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
        Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
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       ,Y. and Hayashizaki,Y.
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      system. Genome Res. 9 (5), 463-470 (1999)
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        Please visit our web site (http://genome.rtc.riken.go.jp) for
      further details.
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    AUTHOR (AU):
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                                        contributed to prepare mouse
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                                        primed with a primer [5
                                        GAGAGAGAAGGATCCAAGAGCTCTTTTTTTT
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                                        by using trehalose
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                                        round of normalization to Rot = 10.0 and subtraction to Rot =
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 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.
 Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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DEFINITION (DEF):

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NUCLEIC ACID COUNT (NA): 73 a

Tel: 81-45-503-9222 Fax: 81-45-503-9216

Contact: Yoshihide Hayashizaki

Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/

AV335961

193

AV335961.1

248628-93-5

mRNA; linear

11 Nov 1999

house mouse.

Mus musculus

32 c

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)

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Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
      ,Y. and Hayashizaki,Y.
       Automated filtration-based high-throughput plasmid preparation
      system. Genome Res. 9 (5), 463-470 (1999)
       Carninci, P. and Hayashizaki, Y.
       High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
      19-44 (1999)
       Please visit our web site (http://genome.rtc.riken.go.jp) for
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REFERENCE:
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                             Konno, H.; Aizawa, K.; Akahira, S.; Akiyama, J.; Carninci, P.; Endo, T.; Fukuda, S.; Fukunishi, Y.; Hara, A.; Hayatsu, N.; Hirozane, T.; Hori, F.; Ishii, Y.;
   AUTHOR (AU):
                             Ishikawa,T.; Itoh,M.; Izawa,M.; Kadota,K.; Kagawa,I.; Kai,C.?; Kawai,J.; Kikuchi,N.; Kojima,Y.; Koya,S.;
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NUCLEIC ACID COUNT (NA): 105 a
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COMMENT:
      Contact: Yoshihide Hayashizaki
      Laboratory for Genome Exploration Research Group, RIKEN Genomic
      Sciences Center(GSC), Yokohama Institute
      The Institute of Physical and Chemical Research (RIKEN)
      1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
      Tel: 81-45-503-9222
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      Email: genome-res@gsc.riken.go.jp,
      URL:http://genome.gsc.riken.go.jp/
      Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
       Transcriptional sequencing: A method for DNA sequencing using RNA
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       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                          tissues. 1st strand cDNA was
                                          primed with a primer [5
                                          GAGAGAGAAGGATCCAAGAGCTCTTTTTTTT
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 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
  1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Email: genome-res@gsc.riken.go.jp,
 URL:http://genome.gsc.riken.go.jp/
 Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.
 Matsuura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki
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DATE (DATE):

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MOLECULE TYPE (CI):

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ORGANISM (ORGN):

GenBank ACC. NO. (GBN): AV321727

NUCLEIC ACID COUNT (NA): 84 a

Tel: 81-45-503-9222 Fax: 81-45-503-9216

Contact: Yoshihide Hayashizaki

AV321727

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AV321727.1

247815-00-5

mRNA: linear

9 Nov 1999

house mouse.

Mus musculus

46 c

Transcriptional sequencing: A method for DNA sequencing using RNA

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polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
       Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.
      Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
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       Please visit our web site (http://genome.rtc.riken.go.jp) for
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REFERENCE:
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SOURCE:
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       Contact: Yoshihide Hayashizaki
       Laboratory for Genome Exploration Research Group, RIKEN Genomic
       Sciences Center(GSC), Yokohama Institute
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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    AUTHOR (AU):
                                  Salto, H., Santo, M.; Salto, K.; Shibata, K.; Shibata, Y.; Shigemoto, Y.; Shiraki, T.; Sogabe, Y.; Sugahara, Y.; Suzuki, H.; Suzuki, H.; Takahashi, F.; Tateno, M.; Tominaga, N.; Tsunoda, Y.; Watahiki, A.; Watanabe, S.; Yamamura, T.; Yasunishi, A.; Yokota, T.; Yoshiki, A.; Yoshino, M.; Muramatsu, M.; Hayashizaki, Y. RIKEN Mouse (1000)
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                                          /note="Site-1: SalI; Site-2:
                                          BamHI; cDNA library was prepared
                                          and sequenced in Mouse Genome
                                          Encyclopedia Project of Genome
                                          Exploration Research Group in
                                          Riken Genomic Sciences Center and
                                          Genome Science Laboratory in
                                          RIKEN. Division of Experimental
                                          Animal Research in Riken
                                          contributed to prepare mouse
                                          tissues. 1st strand cDNA was
                                          primed with a primer [5'
                                          GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTT
                                          TTTTTTVN 3'], cDNA was prepared
                                          by using trehalose
                                          thermo-activated reverse
                                          transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                          GAGAGAGATTCTCGAGTTAATTAAATTAATCC
                                          CCCCCCCCC 3']. cDNA was cloned
                                          into the XhoI and BamHI sites.
                                          Vector: a modified pBluescript
                                          KS(+) after bulk excision from
                                          Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
  f 1 atgttcttat ctaaacttct taatttaata cactaaagaa gaagaatgaa acaaagaaga
 61 aagatcagag agagagagaa atattacaag gttgaaaaca aatcttggtg aaaagaagat
121 ttaacctgcg ggttacaaaa aaaaatagtt cacacattgc aaattagtga aaacttggat
181 tectattaca atcatgaett taaatttatt agttaaaatt aaacettatt
                          GENBANK.RTM. COPYRIGHT 2004 on STN
                                      GenBank (R)
                                    GI:6018121
                       Rattus norvegicus growth factor receptor binding
                       protein GRB7 (Grb7) mRNA, complete cds.
                       Norway rat.
Rattus norvegicus
                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                       Euteleostomi; Mammalia; Euthéria; Rodentia;
                       Sciurognathi; Muridae; Murinae; Rattus
                                           548 g
                                                    462 t
                           (bases 1 to 2052)
                       Kasus-Jacobi,A.; Perdereau,D.; Auzan,C.; Clauser,E.;
                       Van Obberghen,E.; Mauvais-Jarvis,F.; Girard,J.;
                       Burnol,A.F.
Identification of the rat adapter
                                                                ***Grb14***
                                                                                as an
                       inhibitor of insulin actions
J. Biol. Chem., 273 (40), 26026-26035 (1998)
                           (bases 1 to 2052)
                       Kasus-Jacobi,A.; Bereziat,V.; Perdereau,D.; Girard,J.;
                       Evidence for an interaction between the insulin
                       receptor and Grb7. A role for two of its binding
                       domains, PIR and SH2
Oncogene, 19 (16), 2052-2059 (2000)
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SEQUENCE (SEQ):

LOCUS (LOC):

DATE (DATE):

SOURCE:

REFERENCE:

REFERENCE:

REFERENCE:

ANSWER 132 OF 156

GenBank VERSION (VER):

CAS REGISTRY NO. (RN):

SEQUENCE LENGTH (SQL):

MOLECULE TYPE (CI):

DIVISION CODE (CI):

DEFINITION (DEF):

ORGANISM (ORGN):

AUTHOR (AU):

TITLE (TI):

JOURNAL (SO): OTHER SOURCE (OS):

AUTHOR (AU):

TITLE (TI):

JOURNAL (SO): OTHER SOURCE (OS):

AUTHOR (AU):

GenBank ACC. NO. (GBN): AF190121

NUCLEIC ACID COUNT (NA): 440 a

AF190121

2052

Rodents

AF190121.1

244113-77-7

mRNA; linear

22 Nov 2000

CA 130:20710

Burnol, A.F.

CA 133:69252

(bases 1 to 2052)

Burnol, A.F.; Perdereau, D.; Kasus-Jacobi, A.

602 c

L2

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (27-SEP-1999) UPR 1524, CNRS, 9 rue Jules

Hetzel, Meudon 92190, France

FEATURES (FEAT):

Feature Key Location Qualifier 1..2052 /organism="Rattus norvegicus" source /db-xref="taxon:10116" /tissue-type="liver' /gene="Grb7" /gene="Grb7" 1..2052 gene 50..1657 CDS /note="molecular adapter" /codon-start=1 /product="growth factor receptor binding protein GRB7" /protein-id="AAF01776.1" /db-xref="GI:6018122' translation="MELDLSPSHLSSSPEDVCPT" **PGTPPETPPPDNPPPGDVKRSQP** LPIPSSRKLREEEFQATSLPSIPNPFPELCSPPS QKPILGGSSGARGLLPRDSSRLCV VKVYSEDGACRSVEVAAGATARHVCEMLVQRAHA LSDENWGLVECHPYLALERGLEDH ESVVEVQEAWPVGGDSRFIFRKNFAKYELFKSPP HTLFPEKMVSSCLDTPTGISHEDL IQNFLNAGSFPEIQGFLQLRGSGRGSGRKLWKRF **FCFLRRSGLYYSTKGTSKDPRHLQ** YVADINESNVYVVTQGRKLYGIPTDFGFCVKPNK LRNGHKGLHIFCSEDEQSRTCWLS AFRLFKYGVQLYKNYQQAQSRHLRLSYLGSPPLR SVSDNTLVAMDFSGHAGRVIENPQ EALSAATEEAQAWRKKTNHRLSLPTPCSGLSLSA AIHRTQPWFHGRISREESQRLIGQ

QGLVDGVFLVRESQRNPQGFVLSLCHLQKVKHYL

ILPSEDEGCLYFSMDDGQTRFTDL LQLVEFHQLNRGILPCLLRHCCARVAL"

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GenBank ACC. No. (GBN): AI928176
GenBank VERSION (VER):
                         AI928176.1 GI:5664140
CAS REGISTRY NO. (RN):
                         241373-88-6
SEQUENCE LENGTH (SQL):
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MOLECULE TYPE (CI):
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DIVISION CODE (CI):
                         Expressed sequence tag
DATE (DATE):
                         8 Mar 2000
DEFINITION (DEF):
                         wo95a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
                         IMAGE:2463064 3' similar to TR:Q14449 Q14449
***GRB14*** . ;, mRNA sequence.
                                         . ;, mRNA sequence.
SOURCE:
 ORGANISM (ORGN):
                         Homo sapiens
                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                          Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                          Hominidae; Homo
NUCLEIC ACID COUNT (NA): 90 a
                                  54 c
                                         48 q
                                                 127 t
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
     Emmert-Buck, M.D., Ph.D.
      cDNA Library Preparation: M. Bento Soares, Ph.D.
      cDNA Library Arrayed by: Greg Lennon, Ph.D.
      DNA Sequencing by: Washington University Genome Sequencing Center
      Clone distribution: NCI-CGAP clone distribution information can be
     found through the I.M.A.G.E. Consortium/LLNL at:
     www-bio.llnl.gov/bbrp/image/image.html
     Insert Length: 399
                           Std Error: 0.00
     Seq primer: -40UP from Gibco.
REFERENCE:
                         1 (bases 1 to 319)
   AUTHOR (AU):
                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                         National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
   TITLE (TI):
                         Unpublished (1997)
   JOURNAL (SO):
FEATURES (FEAT):
  Feature Key
                     Location
                                               Oualifier
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                                          NCI-CGAP-Kid3 was prepared, and ss
                                           circles were made in vitro.
                                           Following HAP purification, this
                                           DNA was used as tracer in a
                                           subtractive hybridization
                                           reaction. The driver was PCR-amplified cDNAs from a pool of
                                           5,000 clones made from the same
                                           library (cloneIDs 1322376-1323911, 1456007-1456775, and
                                           1500552-1502855). Subtraction by
                                           Bento Soares and M. Fatima
                                           Bonaldo.
SEQUENCE (SEQ):
     1 ttcctaaggt ttaattttaa ctaatgaatt ttaaatgatg aatgtaaagt caatccaagt
    61 ctttgctťat ttgcaatgca caaacťattt ttttgtaacť tgcaggtgaa atacattcťt
   121 ttcacatgat aaigttticg cccttattta tggtctttta tiatiitict tgagtccttt
   181 teetteaata giitaataag teaetietgg etigietaga gageaateet ageacaataa
   241 tgtttcaact tgcaaggaag aacgccctta ttgagttgat agaactccac cagctgtatt
   301 agatctgtaa atcttgtgt
L2
     ANSWER 134 OF 156
                           GENBANK, RTM. COPYRIGHT 2004 on STN
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LOCUS (LOC):

GenBank ACC. NO. (GBN): AI870172

AI870172

GenBank (R)

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GenBank VERSION (VER):
                            AI870172.1 GI:5544140
 CAS REGISTRY NO. (RN):
                            390159-63-4
 SEQUENCE LENGTH (SQL):
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 MOLECULE TYPE (CI):
                            mRNA; linear
 DIVISION CODE (CI):
                            Expressed sequence tag
 DATE (DATE):
                            7 Mar 2000
                            wll5e05.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2424992 3' similar to TR:Q14449 Q14449
 DEFINITION (DEF):
                              ***GRB14*** . ;, mRNA sequence.
 SOURCE:
 ORGANISM (ORGN):
                            Homo sapiens
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                            Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                            Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 189 a
                                      157 c
                                               145 q
                                                        249 t
                                                                 5 others
 COMMENT:
      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs-r@mail.nih.gov
      Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
      Emmert-Buck, M.D., Ph.D.
       CDNA Library Preparation: Life Technologies, Inc.
       CDNA Library Arrayed by: Greg Lennon, Ph.D.
       DNA Sequencing by: Washington University Genome Sequencing Center
       Clone distribution: NCI-CGAP clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      www-bio.llnl.gov/bbrp/image/image.html
      Insert Length: 1767
                              Std Error: 0.00
      Seq primer: -40UP from Gibco
      High quality sequence stop: 414.
REFERENCE:
                               (bases 1 to 745)
    AUTHOR (AU):
                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
    TITLE (TI):
                           National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
    JOURNAL (SO):
                           Unpublished (1997)
FEATURES (FEAT):
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                     Location
                                                  Qualifier
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                                              /lab-host="DH10B"
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                                              size 1.75 kb. Life Technologies
                                              catalog #: 11538-014
SEQUENCE (SEQ):
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   121 tcacatggta atgttttcgc ccttatttat ggtcttttat tattttctt gagtcctttt
   181 ccttcaatag tttaaataag tcaccttctg ggcttgtcta gagagcaatc ctagcacaat 241 aatgtttcaa cttgcaagga agaacgccct tattgagttg atagaactcc accagctgta
   301 ttagatctgt aaatcttgtg tggccatcat ccagtgtgtg gaacatttca ccgtcatctt 361 ctactggtat aatttgaaag tgctttattt tttgtccatg actcattgac agtacgaaag 421 ttttggggtt actctgacta tcccgtacca agaaaactcc atccacaagt ccttgctgaa
   481 taatcaatcg ctgagcctca tctctagaaa tnttgtggtg aaaccatggc tgggaccggt
   541 ggatagccat gtntgtggca gagctctgtg aagagcagtg gggctaccgt gagtgcccag
601 gcgtaaacat cctttttnc tccaagcgag tccctcttca accgcaactg aaaggggctt
   661 ccgtgggatn ttctaatact ctgctťtťcc tgccctgaga agtčattgcť accagggaaa
   721 tctctgtnta cctcctcata ggtga
L2
     ANSWER 135 OF 156
                             GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                           AI767914
                                          GenBank (R)
GenBank ACC. No. (GBN): AI767914
GenBank VERSION (VER):
                           AI767914.1 GI:5234435
CAS REGISTRY NO. (RN):
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SEQUENCE LENGTH (SQL):
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MOLECULE TYPE (CI):
                           mRNA; linear
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DIVISION CODE (CI):
                           Expressed sequence tag
DATE (DATE):
                           21 Dec 1999
DEFINITION (DEF):
                           wi99c10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone
                           IMAGE:2401458 3' similar to TR:Q14449 Q14449

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SOURCE:
                           human.
 ORGANISM (ORGN):
                           Homo sapiens
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                           Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                           Hominidae; Homo
: 112 a 74 c
NUCLEIC ACID COUNT (NA): 112 a
                                            74 g
                                                    168 t
                                                             1 others
COMMENT:
      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs-r@mail.nih.gov
      Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
      Emmert-Buck, M.D., Ph.D.
       CDNA Library Preparation: M. Bento Soares, Ph.D.
       CDNA Library Arrayed by: Greg Lennon, Ph.D.
      DNA Sequencing by: Washington University Genome Sequencing Center
      Clone distribution: NCI-CGAP clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
     www-bio.lln1.gov/bbrp/image/image.html
      Insert Length: 925
                            Std Error: 0.00
      Seg primer: -40UP from Gibco
     High quality sequence stop: 260.
REFERENCE:
                              (bases 1 to 429)
   AUTHOR (AU):
                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                          National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
Unpublished (1997)
   TITLE (TI):
   JOURNAL (SO):
FEATURES (FEAT):
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                      Location
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                                            NCI-CGAP-Kid5 was prepared, and ss
                                            circles were made in vitro.
                                            Following HAP purification, this
                                            DNA was used as tracer in a
                                            subtractive hybridization
                                            reaction. The driver was PCR-amplified cDNAs from a pool of
                                            5,000 clones made from the same
                                            library (cloneIDs 1323912-1325831,
1471368-1472903 and
                                            1492104-1493255). Subtraction by
                                            Bento Soares and M. Fatima
                                            Bonaldo.
SEQUENCE (SEQ):
     1 ttttcctaag gtttaatttt aactaatgaa ttttaaatga tgaatgtaaa gtcaatccaa
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   181 tttccttcaa tagtttaata agtcacttct ggcttgtcta gagagcaatc ctagcacaat
   241 aatgtttcaa cttgcaagga agaacgccct tattgagttg atagaactcc accagctgtt
   301 ttagatctgt aatīttgggg tggccatatc caggtgtgtg gaacatttca ccgtcatctt
   361 ctactggtat aattggaaaa gigcittait niittgicca igacicitgg accgiaccaa
   421 agttttggg
L2
     ANSWER 136 OF 156
                            GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
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                                        GenBank (R)
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GenBank VERSION (VER): AI760945.1 GI:5176612
CAS REGISTRY NO. (RN): 236076-02-1
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MOLECULE TYPE (CI):
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DATE (DATE):
                           21 Dec 1999
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SOURCE:
                           human.
 ORGANISM (ORGN):
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                           Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                           Hominidae; Homo
NUCLEIC ACID COUNT (NA): 90 a
                                   54 c
                                           46 g
                                                   122 t
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
      Emmert-Buck, M.D., Ph.D.
       cDNA Library Preparation: M. Bento Soares, Ph.D.
       cDNA Library Arrayed by: Greg Lennon, Ph.D.
      DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
     found through the I.M.A.G.E. Consortium/LLNL at:
     www-bio.llnl.gov/bbrp/image/image.html
     Insert Length: 403
                            Std Error: 0.00
     Seq primer: -40UP from Gibco.
REFERENCE:
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   AUTHOR (AU):
                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                          National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
Unpublished (1997)
   TITLE (TI):
   JOURNAL (SO):
FEATURES (FEAT):
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                                            (clear cell type)
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pT7T3D-Pac (Pharmacia) with a
                                            modified polylinker; Site-1: Not
                                            I; Site-2: Eco RI; Plasmid DNA
                                            from the normalized library
                                            NCI-CGAP-Kid5 was prepared, and ss
                                            circles were made in vitro.
                                            Following HAP purification, this
                                            DNA was used as tracer in a
                                            subtractive hybridization
                                            reaction. The driver was PCR-amplified cDNAs from a pool of
                                            5,000 clones made from the same
                                            library (cloneIDs 1323912-1325831,
                                            1471368-1472903 and
                                            1492104-1493255). Subtraction by
                                            Bento Soares and M. Fatima
                                            Bonaldo.
SEQUENCE (SEQ):
    1 tttcctaagg tttaatttta actaatgaat tttaaatgat gaatgtaaag tcaatccaag 61 tctttgctta tttgcaatgc acaaactatt tttttgtaac ttgcaggtga aatacattct
   121 tttcacatga taacgttttc gcccttattt atggtctttt attattttc ttgagtcctt
   181 ttccttcaat agtttaataa gtcacttctg gcttgtctag agagcaatcc tagcacaata
   241 atgittcaac tigcaaggaa gaacgcccii attgagitga tagaactcca ccagcigtat
   301 tagatctgta aa
L2
     ANSWER 137 OF 156
                            GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                          AI695260
                                         GenBank (R)
GenBank ACC. NO. (GBN): A1695260
GenBank VERSION (VER): A1695260.1 GI:4983160
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SEQUENCE LENGTH (SQL):
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DIVISION CODE (CI):
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SOURCE:
 ORGANISM (ORGN):
                          Homo sapiens
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                          Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                          Hominidae; Homo
                                    82 c
NUCLEIC ACID COUNT (NA): 112 a
                                           62 g
                                                   152 t
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
     Emmert-Buck, M.D., Ph.D.
      cDNA Library Preparation: M. Bento Soares, Ph.D.
      cDNA Library Arrayed by: Greg Lennon, Ph.D.
      DNA Sequencing by: Washington University Genome Sequencing Center
      Clone distribution: NCI-CGAP clone distribution information can be
     found through the I.M.A.G.E. Consortium/LLNL at:
     www-bio.lln1.gov/bbrp/image/image.html
     Insert Length: 848
                            Std Error: 0.00
     Seq primer: -40UP from Gibco
     High quality sequence stop: 396.
                             (bases 1 to 408)
REFERENCE:
                          1
                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
   AUTHOR (AU):
   TITLE (TI):
                          National Cancer Institute, Cancer Genome Anatomy
                          Project (CGAP), Tumor Gené Index
Unpublished (1997)
   JOURNAL (SO):
FEATURES (FEAT):
  Feature Key
                      Location
                                                Qualifier
 /organism="Homo sapiens"
                 1..408
                                            /db-xref="taxon:9606"
                                            /clone="IMAGE:2296887"
                                            /clone-lib="NCI-CGAP-Kid11"
                                            /lab-host="DH10B"
                                            /note="Organ: kidney; Vector:
pT7T3D-Pac (Pharmacia) with a
                                            modified polylinker; Site-1: Not
I; Site-2: Eco RI; Plasmid DNA
                                            from the normalized library
                                            NCI-CGAP-Kid3 was prepared, and ss
                                            circles were made in vitro.
                                            Following HAP purification, this
                                            DNA was used as tracer in a
                                            subtractive hybridization
                                            reaction. The driver was
PCR-amplified cDNAs from a pool of
5,000 clones made from the same
                                            library (cloneIDs 1322376-1323911,
                                            1456007-1456775, and
                                            1500552-1502855). Subtraction by
                                            Bento Soares and M. Fatima
                                            Bonaldo.
SEQUENCE (SEO):
     1 tcctaaggtt taattttaac taatgaattt taaatgatga atgtaaagtc aatccaagtc
   61 tttgcttatt tgcaatgcac aaactatttt tttgtaactt gcaggtgaaa tacattcttt 121 tcacatgata atgttttcgc ccttatttat ggtcttttat tatttttctt gagtcctttt 181 ccttcaatag tttaataagt cacttctggc ttgtctagag agcaatccta gcacaataat
   241 gtttcaacti gcaaggaaga acgccctiat tgagttgata gaactccacc agctgtatta
   301 gatetgtaaa tettgtgtgg ceateateea gtgtgtggaa eattteaceg teatetteta
   361 cccatccaca agtccttgct gaataatcaa tcgctgagcc tcatctta
L2
     ANSWER 138 OF 156
                            GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                          AI671320
                                         GenBank (R)
GenBank ACC. No. (GBN): AI671320
GenBank VERSION (VER):
                          AI671320.1 GI:4851051
CAS REGISTRY NO. (RN):
                          232699-27-3
SEQUENCE LENGTH (SQL):
                          497
MOLECULE TYPE (CI):
                          mRNA: linear
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DIVISION CODE (CI):
                             Expressed sequence tag
DATE (DATE):
                             17 Dec 1999
DEFINITION (DEF):
                             wc29a02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
                             IMAGE:2316554 3' similar to TR:Q14449 Q14449 ***GRB14*** .;, mRNA sequence.
SOURCE:
                              human.
 ORGANISM (ORGN):
                             Homo sapiens
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                             Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                             Hominidae; Homo
NUCLEIC ACID COUNT (NA): 144 a
                                        100 c
                                                  87 g
                                                           164 t
                                                                     2 others
COMMENT:
      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs-r@mail.nih.gov
      Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
      Emmert-Buck, M.D., Ph.D.
       cDNA Library Preparation: M. Bento Soares, Ph.D.
       cDNA Library Arrayed by: Greg Lennon, Ph.D.
       DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      www-bio.llnl.gov/bbrp/image/image.html
      Insert Length: 795
                               Std Error: 0.00
      Seg primer: -40UP from Gibco
      High quality sequence stop: 372.
                             1 (bases 1 to 497)
REFERENCE:
   AUTHOR (AU):
                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
    TITLE (TI):
                             National Cancer Institute, Cancer Genome Anatomy
                             Project (CGAP), Tumor Gene Index
Unpublished (1997)
    JOURNAL (SO):
FEATURES (FEAT):
  Feature Key
                        Location
                                                      Qualifier
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source
                   1..497
                                                 /organism="Homo sapiens"
                                                 /db-xref="taxon:9606"
                                                 /clone="IMAGE:2316554"
/clone-lib="NCI-CGAP-Kid11"
                                                 /lab-host="DH10B"
                                                 /note="Organ: kidney; Vector:
pT7T3D-Pac (Pharmacia) with a
                                                 modified polylinker; Site-1: Not
I; Site-2: Eco RI; Plasmid DNA
                                                 from the normalized library
                                                 NCI-CGAP-Kid3 was prepared, and ss
                                                 circles were made in vitro.
                                                 Following HAP purification, this
                                                 DNA was used as tracer in a
                                                 subtractive hybridization
                                                 reaction. The driver was PCR-amplified cDNAs from a pool of
                                                 5,000 clones made from the same
                                                 library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by
                                                 Bento Soares and M. Fatima
                                                 Bonaldo.
SEQUENCE (SEQ):
   1 gcctgccagt gacacataaa tatcactatt gccaaattcg ctaaaaactg caaatgccgc 61 ggttcctttg atgttccttt agtagaaaaa tataaaccag atcttcttag aaaaaagtaa 121 attttttcc aagacttctt tccctgttct ttcgcatgta agaaaccatg aatttcagga 181 tatgtgcttg aactcagaaa catctgcaaa atctgtgtgg gggatatttc accattggtt tcagttgcaa aagataccat atgctctgga aaaaaataca ttgggtttt aaagaactca
   301 tatitggcat aaitttttct aaagtatagt ttgttttctt cticiatccc ccagttggat
   361 agcacttcaa tcaccagttc gtggtcttct attgttcttt ctacacctat gtgaggcagg
   421 tgctcanaaa gggtccagct gtggtcatca atgtaatgat tcttcaggat caacagctga
   481 ncaacatctc gagccgt
L2
     ANSWER 139 OF 156
                               GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                             AI624682
                                             GenBank (R)
GenBank ACC. NO. (GBN): AI624682
GenBank VERSION (VER): A1624682.1 GI:4649613
CAS REGISTRY NO. (RN): 230649-94-2
SEQUENCE LENGTH (SQL): 533
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MOLECULE TYPE (CI):
                         mRNA; linear
DIVISION CODE (CI):
                         Expressed sequence tag
DATE (DATE):
                         14 Dec 1999
DEFINITION (DEF):
                         ts43e12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone
                         IMAGE:2231374 3' similar to TR:Q14449 Q14449
                           ***GRB14***
                                        . ;, mRNA sequence.
SOURCE:
 ORGANISM (ORGN):
                         Homo sapiens
                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                         Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                         Hominidae; Homo
NUCLEIC ACID COUNT (NA): 144 a
                                  104 c
                                           91 q
                                                  193 t
                                                          1 others
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
     Emmert-Buck, M.D., Ph.D.
      CDNA Library Preparation: Life Technologies, Inc.
      CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
      Clone distribution: NCI-CGAP clone distribution information can be
     found through the I.M.A.G.E. Consortium/LLNL at:
     www-bio.llnl.gov/bbrp/image/image.html
     Insert Length: 1696
                           Std Error: 0.00
     Seq primer: -40UP from Gibco
     High quality sequence stop: 401
     POLYA=No.
REFERENCE:
                         1 (bases 1 to 533)
   AUTHOR (AU):
                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                         National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
   TITLE (TI):
                         Unpublished (1997)
   JOURNAL (SO):
FEATURES (FEAT):
  Feature Key
                    Location
                                              Qualifier
/organism="Homo sapiens"
source
                1..533
                                          /db-xref="taxon:9606"
                                          /clone="IMAGE:2231374"
                                          /clone-lib="NCI-CGAP-Ut1"
/tissue-type="well-differentiated
                                          endometrial adenocarcinoma, 7
                                          pooled tumors"
                                          /lab-host="DH10B"
                                          /note="Organ: uterus; Vector:
                                          pCMV-SPORT6; Site-1: SalI; Site-2:
                                          NotI; Cloned unidirectionally.
                                          Primer: Oligo dT. Average insert
                                          size 1.75 kb. Life Technologies
                                          catalog #: 11538-014
SEQUENCE (SEQ):
     1 tcctaaggtt taattttaac taatgaattt taaatgatga atgtaaagtc aatccaagtc
    61 tttgcttatt tgcaatgcac aaactatttt tttgtaactt gcaggtgaaa tacattcttt
   121 tcacatggta atgttticgc ccttatttat ggtcttttat tatittictt gagtcctttt
   181 ccttcaatag tttaataagt cacttctggc ttgtctagag agcaatccta gcacaataat
   241 gtttcaactt gcaaggaaga acgcccttat tgagttgata gaactccacc agctgtatta
   301 gatetgtaaa tettgtgtgg eeateateea gtgtgtggaa eattteaceg teatetteta
   361 ctggtataat ttgaaagtgc tttatttttt gtccatgact cattgacagt acgaaagttt
   421 tggggttact ctgactatcc cgtaccaaga aaactccatc cacaagtcct tgctgaataa
   481 tcaatcgctg agcctcatct ctagaaatnt tgtgtgaacc atggctggga ccg
L2
     ANSWER 140 OF 156
                           GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                         AI610228
                                      GenBank (R)
GenBank ACC. NO. (GBN): AI610228
GenBank VERSION (VER):
                         AI610228.1 GI:4619395
                         390132-63-5
CAS REGISTRY NO. (RN):
SEQUENCE LENGTH (SQL):
                         701
MOLECULE TYPE (CI):
DIVISION CODE (CI):
                         mRNA; linear
                         Expressed sequence tag
DATE (DATE):
                         13 May 1999
                         tp15g09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone
DEFINITION (DEF):
                         IMAGE: 2187904 3' similar to TR: Q14449 Q14449
                           ***GRB14*** . ;, mRNA sequence.
SOURCE:
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ORGANISM (ORGN):
                            Homo sapiens
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                            Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                            Hominidae; Homo
NUCLEIC ACID COUNT (NA): 179 a
                                      144 c
                                               132 g
                                                        242 t
                                                                 4 others
COMMENT:
      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs-r@mail.nih.gov
      Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
      Emmert-Buck, M.D., Ph.D.
       cDNA Library Preparation: Life Technologies, Inc.
       cDNA Library Arrayed by: Greg Lennon, Ph.D.
       DNA Sequencing by: Washington University Genome Sequencing Center
       Clone distribution: NCI-CGAP clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      www-bio.lln1.gov/bbrp/image/image.html
      Insert Length: 803
                            Std Error: 0.00
      Seq primer: -40UP from Gibco
      High quality sequence stop: 406
      POLYA=No.
REFERENCE:
                            1 (bases 1 to 701)
                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
   AUTHOR (AU):
   TITLE (TI):
                           National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
   JOURNAL (SO):
                            Unpublished (1997)
FEATURES (FEAT):
  Feature Key
                       Location
                                                  Qualifier
 1..701
                                              /organism="Homo sapiens"
source
                                              /db-xref="taxon:9606
                                              /clone="IMAGE:2187904"
                                              /clone-lib="NCI-CGAP-Gas4"
                                              /tissue-type="poorly
                                              differentiated adenocarcinoma with
                                              signet ring cell features"
/lab-host="DH108"
                                              /note="Organ: stomach; Vector:
                                              pCMV-SPORT6; Site-1: SalI; Site-2:
                                              NotI; Cloned unidirectionally.
                                              Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies
                                              catalog #: 11549-011
SEQUENCE (SEQ):
      1 ttctaaggtt taattttaac taatgaattt taaatgatga atgtaaagtc aatccaagtc
     61 tttgcttatt tgcaatgcac aaactattt tttgtaactt gcaggtgaaa tacattctt
   121 tcacatggta atgttticgc ccttatttat ggtcttttat tattitictt gagtcctttt
   181 ccttcaatag tttaataagt cacttctggc ttgtctagag agcaatccta gcacaataat
   241 gtttcaactt gcaaggaaga acgcccttat tgagttgata gaactccacc agctgtatta 301 gatctgtaaa tcttgtgtgg ccatcatcca gtgtgtggaa catttcaccg tcatcttcta 361 ctggtataat ttgaaagtgc tctattttt gtccatgact cattgacagt acgaaagttt 421 tggggttact ctgactatcc cgtaccaaaa aactccatcc acaagtcctt gctgaataat 481 caatcgctga gcctcatctc tagaaatttt gtggtgaaac catggctggg accggtggat
   541 agccatgttt gtggcagagc tctgtgaaga gcagtggngc taccgtgagt gcccagccgt 601 aaacatcctt ttttncttcc agcgagtcct tcttcaaccg caactgaaag ggcttcagnn
   661 ggattttcta taactctgct tttctggcct gagaagtcca t
L2
     ANSWER 141 OF 156
                              GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                           AI609572
                                          GenBank (R)
GenBank ACC. No. (GBN): AI609572
GenBank VERSION (VER):
                           AI609572.1 GI:4618739
CAS REGISTRY NO. (RN):
                           230319-99-0
SEQUENCE LENGTH (SQL):
                           368
MOLECULE TYPE (CI):
                           mRNA: linear
DIVISION CODE (CI):
                           Expressed sequence tag
DATE (DATE):
                           14 May 1999
DEFINITION (DEF):
                           tw28a08.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone
                           IMAGE:2260982 3' similar to TR:Q14449 Q14449
                              ***GRB14***
                                            . ;, mRNA sequence.
SOURCE:
 ORGANISM (ORGN):
                           Homo sapiens
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                           Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                           Hominidae: Homo
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NUCLEIC ACID COUNT (NA): 100 a
                                   59 c
                                           57 g
                                                 151 t
                                                           1 others
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
     R. Emmert-Buck, M.D., Ph.D.
      cDNA Library Preparation: Life Technologies, Inc.
      cDNA Library Arrayed by: Greg Lennon, Ph.D.
      DNA Sequencing by: Washington University Genome Sequencing Center
     Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
     Insert Length: 318
                           Std Error: 0.00
     Seg primer: -40UP from Gibco
     High quality sequence stop: 324
     POLYA=No.
                          1 (bases 1 to 368)
REFERENCE:
   AUTHOR (AU):
                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
   TITLE (TI):
                          National Cancer Institute, Cancer Genome Anatomy
                          Project (CGAP), Tumor Gene Index
                          Unpublished (1997)
   JOURNAL (SO):
FEATURES (FEAT):
  Feature Key
                     Location
                                                Qualifier
______+
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                 1..368
source
                                           /db-xref="taxon:9606"
                                           /clone="IMAGE:2260982"
                                           /clone-lib="NCI-CGAP-0v35"
                                            /tissue-type="tumor, 5 pooled (see
                                           description)"
                                           /lab-host="DH10B"
                                           /note="Organ: ovary; Vector: pCMV-SPORT6; Site-1: SalI; Site-2:
                                           NotI; This library represents the
                                           normalized version of
                                           NCI-CGAP-Ov23. Cloned
                                           unidirectionally. Primer: Oligo
                                           dT. Average insert size 0.86 kb.
                                           Tumor types include: mixed
                                           Mullerian tumor, papillary serous, clear cell, spindle cell. All are
                                                                         All are
                                           primary tumors, metastasis
                                           positive. Constructed by Life
                                           Technologies."
SEQUENCE (SEQ):
     1 tttttttttt ttttttttt ttttttatgc atacacttct tggatttatt aatgctatag
    61 ttctatgaaa tccatgagta aatatagaaa cattgaaatt ccttctctct ctttagagtt
   121 ttcttggtac gggatagtca gagtaacccc aaaactttcg tactgtcaat gagtcatgga
   181 caaaaaataa agcactttca aattatacca gtaagtaatt cgtgatttca catttgtgta
   241 ttagaaatga ccttaatgct aagcttttga tcttaatgca taagcttttg gaaactttgg 301 ttttcttttg gncttttat taaatataat ttggcagctt gtgctttgac tagagccccg
   361 cgtccgcc
L2
     ANSWER 142 OF 156
                            GENBANK.RTM.
                                           COPYRIGHT 2004 on STN
LOCUS (LOC):
                          AI522272
                                        GenBank (R)
GenBank ACC. NO. (GBN): AI522272
                                       GI:4436407
GenBank VERSION (VER):
                          AI522272.1
                          228602-27-5
CAS REGISTRY NO. (RN):
SEQUENCE LENGTH (SQL): MOLECULE TYPE (CI):
                          604
                          mRNA; linear
DIVISION CODE (CI):
                          Expressed sequence tag
DATE (DATE)
                          13 Apr 1999
DEFINITION (DEF):
                          ti84g01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
                          IMAGE:2138736 3' similar to TR:Q14449 Q14449
                            ***GRB14*** . ;, mRNA sequence.
SOURCE:
                          human.
ORGANISM (ORGN):
                          Homo sapiens
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                          Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                          Hominidae; Homo
NUCLEIC ACID COUNT (NA): 160 a
                                    118 c
                                                     208 t
                                            118 g
COMMENT:
     Contact: Robert Strausberg, Ph.D.
```

```
Email: cgapbs-r@mail.nih.gov
      Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
      Emmert-Buck, M.D., Ph.D.
       cDNA Library Preparation: M. Bento Soares, Ph.D.
       cDNA Library Arrayed by: Greg Lennon, Ph.D.
       DNA Sequencing by: Washington University Genome Sequencing Center
       Clone distribution: NCI-CGAP clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
      Insert Length: 1380
                                Std Error: 0.00
      Seq primer: -40UP from Gibco
      High quality sequence stop: 308.
REFERENCE:
                               (bases 1 to 604)
   AUTHOR (AU):
                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
   TITLE (TI):
                            National Cancer Institute, Cancer Genome Anatomy
                            Project (CGAP), Tumor Gené Index
   JOURNAL (SO):
                            Unpublished (1997)
FEATURES (FEAT):
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  Feature Key
                       Location
 ______
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                  1..604
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                                               /lab-host="DH10B"
                                                /note="Organ: kidney; Vector:
                                               pT7T3D-Pac (Pharmacia) with a
                                               modified polylinker; Site-1: Not
I; Site-2: Eco RI; Plasmid DNA
from the normalized library
                                               NCI-CGAP-Kid3 was prepared, and ss circles were made in vitro.
                                               Following HAP purification, this
                                               DNA was used as tracer in a
                                               subtractive hybridization
                                               reaction. The driver was
                                               PCR-amplified cDNAs from a pool of
                                               5,000 clones made from the same
                                               library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by
                                               Bento Soares and M. Fatima
                                               Bonaldo.
SEQUENCE (SEQ):
      1 ttcctaaggt ttaattttaa ctaatgaatt ttaaatgatg aatgtaaagt caatccaagt
     61 ctttgcttat ttgcaatgca caaactattt ttttgtäact tgcäggtgäa atacattett
   121 ttcacatgat aatgitticg cccttattta tggtčittta třatřítřet tgagiccitt
   181 tccttcaata gtttaataag tcacttctgg cttgtctaga gagcaatcct agcacaataa 241 tgtttcaact tgcaaggaag aacgccctta ttgagttgat agaactccac cagctgtatt 301 agatctgtaa atcttgtgtg gccatcatcc agtgtgtgga acatttcacc gtcatcttct 361 actggtataa tttgaaagtg ctttatttt tgtccatgac tcattgacag tacgaaagtt
   421 ttggggttac tctgactatc ccgtaccaag aaaactccat ccacaagtcc ttgctgaata
   481 atcaatcgct gagcctcatc tctagaaatt ttgtggtgaa accatggctg ggacccgtgg
    541 atagccaīgt ītgītggcaaa gcttcītggaa gaggcāgggg ggcīccīgggā gītgcccaggc
   601 qtaa
      ANSWER 143 OF 156
                               GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                            AI505286
                                            GenBank (R)
GenBank ACC. NO. (GBN): AI505286
GenBank VERSION (VER):
                            AI505286.1 GI:4403137
                            228210-72-8
CAS REGISTRY NO. (RN):
SEQUENCE LENGTH (SQL):
                            578
MOLECULE TYPE (CI):
                            mRNA: linear
DIVISION CODE (CI):
                            Expressed sequence tag
DATE (DATE):
                            11 Mar 1999
DEFINITION (DEF):
                            vp98h08.x1 Stratagene mouse diaphragm (#937303) Mus
                            musculus cDNA clone IMAGE:1092831 3 similar to TR:Q14449 Q14449 ***GRB14*** . ;, mRNA sequence.
SOURCE:
                            house mouse.
 ORGANISM (ORGN):
                            Mus musculus
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                            Euteleostomi; Mammalia; Eutheria; Rodentia;
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Sciurognathi; Muridae; Murinae; Mus

L2

```
NUCLEIC ACID COUNT (NA): 148 a
                                          135 c
                                                     111 g
                                                                179 t
                                                                           5 others
COMMENT:
      Contact: Marra M/WashU-NCI Mouse EST Project 1999
      Washington University School of Medicine
      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
      Tel: 314 286 1800
      Fax: 314 286 1810
      Email: mouseest@watson.wustl.edu
      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
      This clone was previously sequenced on the 5' end only, this new
      data is from the 3' end
      High quality sequence stop: 379.
                                  (bases 1 to 578)
REFERENCE:
                               Marra,M.; Hillier,L.; Kucaba,T.; Martin,J.; Beck,C.;
    AUTHOR (AU):
                               wylie,T.; Underwood,K.; Steptoe,M.; Theising,B.;
                               Allen,M.; Bowers,Y.; Person,B.; Swaller,T.;
Gibbons,M.; Pape,D.; Harvey,N.; Schurk,R.; Ritter,E.;
Kohn,S.; Shin,T.; Jackson,Y.; Cardenas,M.; McCann,R.;
Waterston,R.; Wilson,R.
The WashU-NCI Mouse EST Project 1999
    TITLE (TI):
    JOURNAL (SO):
                               Unpublished (1999)
FEATURES (FEAT):
                         Location
                                                         Qualifier
  Feature Key
  /organism="Mus musculus"
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/clone="IMAGE:1092831"
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                    1..578
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                                                    /tissue-type="diaphragm"
/dev-stage="adult"
                                                     /lab-hosť="SOLR (kanamycin
                                                     resistant)"
                                                     /note="Organ: diaphragm; Vector:
                                                     pBluescript SK-; Site-1: EcoRI;
                                                     Site-2: XhoI; Cloned
                                                     unidirectionally from mRNA
                                                     prepared from diaphragm muscle.
                                                    Primer: Oligo dT. Average insert size: 1.5 kb. Uni-ZAP XR Vector;
                                                    ~5' adaptor sequence: 5'
                                                    GAATTCGGCACGAG 3' ~3' adaptor
                                                     sequence: 5
                                                    CTCGAGTTTTTTTTTTTTTTTTTTTTT
SEQUENCE (SEQ):
      1 aataaggttt aattttaact aataaattta aaggcatgag tgtaatagga atccaagttt
   61 tcactaattt gcaatgtgtg acctatttt ttttgtaacc cgcaggtgaa atcttcttt 121 caccatggtt tgttttcagc cttgtgatct ctctctctc ctctaatcat tctcctttgc 181 atccttcttc ttctgtagtg taacgagtga cacacagttt ggctaaacag ccatcctagc 241 acagtaatgc ttcagcttgc aaggaaggac cccctgttg agctggtaga actccaccag 301 ctggatgagg tctgtgaact tcgtatggc atcatcaga gtatggaaca gctcaccatc
    361 atcītcīacg ggtataatnt galagtgītt tatctttīgt ccatgactca itgacagtac
    421 aaaagttetg gggttactet gactateeeg taccaagaaa actneateea caggeeeetg
    481 ccgaatgate agricgetgag ceteatetet tgaaatrietg tggtgaaace catgttggae
    541 cgātggāaac cātgttcaca ccanaactct ggaagggc
L2
      ANSWER 144 OF 156
                                  GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                               AI494168
                                                GenBank (R)
GenBank ACC. NO. (GBN): AI494168
GenBank VERSION (VER):
                               AI494168.1 GI:4395171
CAS REGISTRY NO. (RN):
                               228132-01-2
SEQUENCE LENGTH (SQL):
                               368
MOLECULE TYPE (CI):
                               mRNA; linear
DIVISION CODE (CI):
                               Expressed sequence tag
                               13 Apr 1999
DATE (DATE):
                               ti14f01.y1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2130457 5' similar to TR:Q14449 Q14449 ***GRB14*** ;, mRNA sequence.
DEFINITION (DEF):
SOURCE:
                               Homo sapiens
 ORGANISM (ORGN):
                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
```

```
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                            Hominidae; Homo
NUCLEIC ACID COUNT (NA): 98 a
                                                      141 t
                                      71 c
                                              58 q
COMMENT:
      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs-r@mail.nih.gov
      Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
      Emmert-Buck, M.D., Ph.D.
       cDNA Library Preparation: M. Bento Soares, Ph.D.
       cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
       Clone distribution: NCI-CGAP clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      www-bio.lln1.gov/bbrp/image/image.html
      Insert Length: 416
                              Std Error: 0.00
      Seq primer: -40RP from Gibco.
REFERENCE:
                               (bases 1 to 368)
   AUTHOR (AU):
                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                            National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
   TITLE (TI):
   JOURNAL (SO):
                            Unpublished (1997)
FEATURES (FEAT):
  Feature Key
                       Location
                                                    oualifier
____________
                                               /organism="Homo sapiens"
                   1..368
source
                                               /db-xref="taxon:9606"
                                                /clone="IMAGE:2130457"
                                               /clone-lib="NCI-CGAP-Kid11"
/lab-host="DH10B"
                                               /note="Organ: kidney; Vector:
pT7T3D-Pac (Pharmacia) with a
                                               modified polylinker; Site-1: Not I; Site-2: Eco RI; Plasmid DNA
                                                from the normalized library
                                               NCI-CGAP-Kid3 was prepared, and ss circles were made in vitro.
                                                Following HAP purification, this
                                               DNA was used as tracer in a
                                                subtractive hybridization
                                               reaction. The driver was PCR-amplified cDNAs from a pool of
                                                5,000 clones made from the same
                                               library (cloneIDs 1322376-1323911, 1456007-1456775, and
                                                1500552-1502855). Subtraction by
                                                Bento Soares and M. Fatima
                                                Bonaldo.
SEQUENCE (SEQ):
   1 tcctaaggtt taattttaac taatgaattt taaatgatga atgtaaagtc aatccaagtc 61 tttgcttatt tgcaatgcac aaactatttt tttgtaactt gcaggtgaaa tacattcttt 121 tcacatgata atgttttcgc ccttatttat ggtcttttat tattttctt gagtccttt
   181 ccttcaatag tttaataagt cacttctggc ttgtctagag agcaatccta gcacaataat
   241 gtttcaactī gcaaggaaga acgcccttat tgagttgata gaactccacc agctgtatta
   301 gatetgtaaa tettgigtgg ceateateea gigigtggaa eattteaceg teatettete
   361 ctcgtgcc
L2
     ANSWER 145 OF 156
                               GENBANK.RTM.
                                               COPYRIGHT 2004 on STN
LOCUS (LOC):
                            AI425417
                                            GenBank (R)
GenBank ACC. NO. (GBN): AI425417
GenBank VERSION (VER):
                            AI425417.1 GI:4271348
CAS REGISTRY NO. (RN):
                            226504-01-4
SEQUENCE LENGTH (SQL):
                            503
                            mRNA; linear
MOLECULE TYPE (CI):
DIVISION CODE (CI):
                            Expressed sequence tag
DATE (DATE):
                            15 Mar 2000
                            my18a09.y1 Barstead mouse heart MPLRB3 Mus musculus cDNA clone IMAGE:696184 5' similar to TR:Q14449 Q14449 ***GRB14*** . ; mRNA sequence.
DEFINITION (DEF):
                                              . ;, mRNA sequence.
SOURCE:
                            house mouse.
 ORGANISM (ORGN):
                            Mus musculus
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                            Euteleostomi; Mammalia; Eutheria; Rodentia;
```

Sciurognathi; Muridae; Murinae; Mus

```
NUCLEIC ACID COUNT (NA): 103 a 171 c
                                                  143 q
                                                            86 t
COMMENT:
      Contact: Marra M/WashU-NCI Mouse EST Project 1999
      Washington University School of Medicine
      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
      Tel: 314 286 1800
      Fax: 314 286 1810
      Email: mouseest@watson.wustl_edu
      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
      correct orientation)
      MGI:429744
      Seq primer: -40RP from Gibco
      High quality sequence stop: 493
      POLYA=No.
REFERENCE:
                             1 (bases 1 to 503)
                             Marra,M.; Hillier,L.; Kucaba,T.; Martin,J.; Beck,C.; Wylie,T.; Underwood,K.; Steptoe,M.; Theising,B.; Allen,M.; Bowers,Y.; Person,B.; Swaller,T.; Gibbons,M.; Pape,D.; Harvey,N.; Schurk,R.; Ritter,E.;
   AUTHOR (AU):
                             Kohn, S.; Shin, T.; Jackson, Y.; Cardenas, M.; McCann, R.;
                             Waterston, R.; Wilson, R.
    TITLE (TI):
                             The WashU-NCI Mouse EST Project 1999
    JOURNAL (SO):
                             Unpublished (1999)
FEATURES (FEAT):
                        Location
                                                      Qualifier
  Feature Key
______+__+__+___+___
                                                 /organism="Mus musculus"
            1..503
                                                 /strain="BALB/c"
/db-xref="taxon:10090"
                                                 /clone="IMAGE:696184"
                                                 /clone-lib="Barstead mouse heart
                                                 MPLRB3"
                                                 /sex="mixed"
                                                 /tissue-type="heart"
/dev-stage="6 weeks"
/lab-host="DH10B"
                                                 /note="Organ: heart; Vector:
                                                 pT7T3D-Pac (Pharmacia) with a
                                                 modified polylinker; Site-1: ECORI; Site-2: NotI; 1st strand
                                                 cDNA was primed with a Not I -
                                                 oligo(dT) primer [5'
                                                 TGTTACGAATCTGAAGTGGGAGCGGCCCCTTT
                                                 to Eco RI adaptors
                                                 [CTTGGATTCGGTACC], digested with Not I and cloned into the Not I and Eco RI sites of the modified
                                                 pT7T3 vector. Library constructed
                                                 by Bob Barstead."
SEQUENCE (SEQ):
      1 aatteggate caaggeaagg egetegetge etgeaacege teggetetge tegeceecag
     61 cccttcgtag ctttcgcctc gcggtcgatg actccctaga cccctggcct acgaccatga
   301 ggagaaaaat gaaagatctg gatgttctgg aaaagccacc cattcccaac ccctttcctg 361 agctctgctg ctctccgctt acatctgtgc tgtcagcagg cctgtttccc agggccaatt
    421 caaggaagaa gcaggtgatt aaagtttaca gcgaggatga aaccagcaga gcattagagg
   481 tgcccagtga catcacagcc cga
L2
      ANSWER 146 OF 156
                                GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                             AI383743
                                             GenBank (R)
GenBank ACC. NO. (GBN): AI383743
GenBank VERSION (VER):
                             AI383743.1 GI:4196524
CAS REGISTRY NO. (RN): SEQUENCE LENGTH (SQL):
                             225333-52-8
                             423
                             mRNA; linear
MOLECULE TYPE (CI):
DIVISION CODE (CI):
                             Expressed sequence tag
```

```
18 Mar 1999
DATE (DATE):
DEFINITION (DEF):
                         tc47e05.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens
                         cDNA clone IMAGE:2067776 3' similar to TR:Q14449 Q14449
                           ***GRB14***
                                         . ;, mRNA sequence.
SOURCE:
                         Homo sapiens
ORGANISM (ORGN):
                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                         Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                         Hominidae; Homo
                                  74 c
NUCLEIC ACID COUNT (NA): 116 a
                                        69 g
                                                 162 t 2 others
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     This clone is available royalty-free through LLNL; contact the
     IMAGE Consortium (info@image.llnl.gov) for further information.
     Insert Length: 967
                          Std Error: 0.00
     Seq primer: -40UP from Gibco.
REFERENCE:
                         1 (bases 1 to 423)
   AUTHOR (AU):
                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                         National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
   TITLE (TI):
                         Unpublished (1997)
   JOURNAL (SO):
FEATURES (FEAT):
  Feature Key
                   Location
                                             Qualifier
/organism="Homo sapiens"
/db-xref="taxon:9606"
/clone="IMAGE:2067776"
                1..423
source
                                          /clone-lib="Soares-total-fetus-Nb2
HF8-9w"
                                          /dev-stage="8-9 weeks"
                                          /lab-host="DH10B"
                                          /note="Vector: pT7T3D-Pac
                                          (Pharmacia) with a modified
                                          polylinker; Site-1: Not I; Site-2:
                                          Eco RI; 1st strand cDNA was
                                          prepared from mRNA obtained from
                                          pooled 8-9 week (total) fetus
                                          material with a Not I - oligo(dT)
                                          primer [5'
                                          TGTTACCĀATCTGAAGTGGGAGCGGCCGCTTAAT
                                          TTTTTTTTTTTTTTT 3'].
                                          Double-stranded cDNA was ligated
                                          to Eco RI adaptors (Pharmacia),
                                          digested with Not I and cloned
                                          into the Not I and Eco RI sites of
                                          the modified pT7T3 vector. Library
                                          went through one round of
                                          normalization, and was constructed
                                          by Bento Soares and M. Fatima Bonaldo. "
SEQUENCE (SEQ):
     1 cctaaggttt aattttaact aatgaatttt aaatgatgaa tgtaaagtca atccaagtct
    61 ttgcttattt gcaatgcaca aactatttt ttgtaacttg caggtgaaat acattctttt
   121 cacatgataa cgttttcgcc cttatttatg gtcttttatt attittcttg agtccttttc
   181 cttcaatagt ttaataagtc acttctggct tgtctagaga gcaatcctag cacaataatg
   241 tttcaacttg caaggaagaa cgcccttatt gagttgatag aactccacca gctgtattag 301 atctgtaaat cttgtgtggc catcatccag tgtgtggaac atttcaccgt catcttctac
   361 tggtátaatt ngaáagtgót ttattnttti gicátgáctc attgacagia caaaagtttt
   421 ggg
                           GENBANK.RTM. COPYRIGHT 2004 on STN
L2
     ANSWER 147 OF 156
LOCUS (LOC):
                         AI364971
                                       GenBank (R)
GenBank ACC. No. (GBN): AI364971
GenBank VERSION (VER):
                         AI364971.1 GI:4124660
                         224494-55-7
CAS REGISTRY NO. (RN):
SEQUENCE LENGTH (SQL):
                         318
MOLECULE TYPE (CI):
                         mRNA; linear
DIVISION CODE (CI):
                         Expressed sequence tag
                         16 Feb 1999
DATE (DATE):
DEFINITION (DEF):
                         qz41h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
                         IMAGE:2029493 3' similar to TR:Q14449 Q14449 ***GRB14*** . ;, mRNA sequence.
```

```
SOURCE:
                          human.
 ORGANISM (ORGN):
                          Homo sapiens
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                          Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                          Hominidae; Homo
NUCLEIC ACID COUNT (NA): 90 a
                                   54 c
                                          48 g
                                                  125 t
                                                           1 others
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D.
      cDNA Library Arrayed by: Greg Lennon, Ph.D.
      DNA Sequencing by: Washington University Genome Sequencing Center
      Clone distribution: NCI-CGAP clone distribution information can be
     found through the I.M.A.G.E. Consortium/LLNL at:
     www-bio.llnl.gov/bbrp/image/image.html
     Insert Length: 447
                            Std Error: 0.00
     Seq primer: -40UP from Gibco.
                          1 (bases 1 to 318)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
REFERENCE:
   AUTHOR (AU):
                          National Cancer Institute, Cancer Genome Anatomy
Project (CGAP), Tumor Gene Index
   TITLE (TI):
                          Unpublished (1997)
   JOURNAL (SO):
FEATURES (FEAT):
                                                Qualifier
  Feature Key
                    Location
____________
                                            /organism="Homo sapiens"
                 1..318
source
                                            /db-xref="taxon:9606
                                            /clone="IMAGE:2029493"
/clone-lib="NCI-CGAP-Kid11"
                                            /lab-host="DH10B"
                                            /note="Organ: kidney; Vector:
                                            pT7T3D-Pac (Pharmacia) with a
                                            modified polylinker; Site-1: Not
                                            I; Site-2: Eco RI; Plasmid DNA
                                            from the normalized library
                                            NCI-CGAP-Kid3 was prepared, and ss circles were made in vitro.
                                            Following HAP purification, this DNA was used as tracer in a subtractive hybridization
                                            reaction. The driver was
                                            PCR-amplified cDNAs from a pool of
                                            5,000 clones made from the same
                                            library (cloneIDs 1322376-1323911, 1456007-1456775, and
                                            1500552-1502855). Subtraction by
                                            Bento Soares and M. Fatima
                                            Bonaldo.
SEQUENCE (SEQ):
     1 ttcctaaggt ttaattttaa ctaatgaatt ttaaatgatg aatgtaaagt caatccaagt
    61 ctttgctťat ttgcaatgca caaacťattt ttttgtaacť tgcaggtgaa atacattcťt
   121 ttcacatgat aatgttticg cccttattta tggnctttta ttattitict tgagtccttt
   181 teetteaata gittaataag teaetteigg etigietaga gageaateet ageacaataa
   241 tgtttcaact tgcaaggaag aacgccctta ttgagttgat agaactccac cagctgtatt
   301 agatctgtaa atcttgtg
L2
     ANSWER 148 OF 156
                            GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                          AI263214
                                        GenBank (R)
GenBank ACC. NO. (GBN): AI263214
GenBank VERSION (VER):
                          AI263214.1 GI:3871417
CAS REGISTRY NO. (RN):
                          221598-25-0
SEQUENCE LENGTH (SQL):
                          382
MOLECULE TYPE (CI):
                          mRNA; linear
DIVISION CODE (CI):
                          Expressed sequence tag
DATE (DATE):
                          3 Feb 1999
DEFINITION (DEF):
                          qz36f04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
                          IMAGE:2028991 3' similar to TR:Q14449 Q14449
                            ***GRB14***
                                          . ;, mRNA sequence.
SOURCE:
                          Homo sapiens
 ORGANISM (ORGN):
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
```

```
Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                           Hominidae; Homo
NUCLEIC ACID COUNT (NA): 112 a
                                     59 c
                                             56 g
                                                   154 t
                                                              1 others
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
     Emmert-Buck, M.D., Ph.D.
       cDNA Library Preparation: M. Bento Soares, Ph.D.
      CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
       Clone distribution: NCI-CGAP clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
     www-bio.lln1.gov/bbrp/image/image.html
     Insert Length: 730
                             Std Error: 0.00
     Seq primer: -40UP from Gibco
     High quality sequence stop: 381.
REFERENCE:
                           1 (bases 1 to 382)
   AUTHOR (AU):
                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                           National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
   TITLE (TI):
                           Unpublished (1997)
   JOURNAL (SO):
FEATURES (FEAT):
  Feature Key
                      Location
                                                  Qualifier
 ___________
                  1..382
                                             /organism="Homo sapiens"
source
                                             /db-xref="taxon:9606"
                                             /clone="IMAGE:2028991"
/clone-lib="NCI-CGAP-Kid11"
/lab-host="DH10B"
                                             /note="Organ: kidney; Vector:
pT7T3D-Pac (Pharmacia) with a
                                             modified polylinker; Site-1: Not
I; Site-2: Eco RI; Plasmid DNA
                                             from the normalized library
                                             NCI-CGAP-Kid3 was prepared, and ss circles were made in vitro.
                                             Following HAP purification, this
                                             DNA was used as tracer in a subtractive hybridization
                                             reaction. The driver was PCR-amplified cDNAs from a pool of
                                             5,000 clones made from the same
                                             library (cloneIDs 1322376-1323911, 1456007-1456775, and
                                             1500552-1502855). Subtraction by
                                             Bento Soares and M. Fatima
                                             Bonaldo.
SEQUENCE (SEQ):
     1 ttttttttt ttttttttt cctaaggttt aattttaact aatgaatttt aaatgatgaa
   61 tgtaaagtca atccaagtct ttgcttattt gcaatgcaca aactatttt ttgtaacttg
121 caggggaaat acattcttt cacatgataa tgttttcgcc cttatttatg gtcttttatt
   181 attiticttg agtccttttc cttcaatagt ttaataagtc acttctggct tgtctagaga
   241 gcaatcctag cacaataatg tttcaactig caaggaaaaa cgccctiatt gagttgatag
   301 aactcacaca cacgcccctt tggggtttta atttttaaa aggaaaaatt tcccggttgg
   361 gggttttnaa aaaaaaaaaa aa
L2
     ANSWER 149 OF 156
                             GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                           AF076619
                                          GenBank (R)
GenBank ACC. NO. (GBN): AF076619
GenBank VERSION (VER):
                           AF076619.1 GI:3650499
CAS REGISTRY NO. (RN):
                           216295-93-1
SEQUENCE LENGTH (SQL):
                           1950
MOLECULE TYPE (CI):
                           mRNA; linear
DIVISION CODE (CI):
                           Rodents
DATE (DATE):
                           26 Sep 1998
DEFINITION (DEF):
                           Rattus norvegicus molecular adapter rGrb14 (
                             ***Grb14*** ) mRNA, complete cds.
SOURCE:
                           Norway rat.
                           Rattus norvegicus
 ORGANISM (ORGN):
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                           Euteleostomi; Mammalia; Eutheria; Rodentia;
                           Sciurognathi; Muridae; Murinae; Rattus
```

```
500 g
NUCLEIC ACID COUNT (NA): 546 a 460 c
                                                                444 t
REFERENCE:
                               1 (bases 1 to 1950)
    AUTHOR (AU):
                               Kasus-Jacobi,A.; Perdereau,D.; Auzan,C.; Clauser,E.;
                               Van Obberghen,E.; Mauvais-Jarvis,F.; Girard,J.;
    TITLE (TI):
                               Identification of the rat adapter ***Grb14***
                                                                                                as an
                               inhibitor of insulin actions
    JOURNAL (SO):
                               J. Biol. Chem., 273 (40), 26026-26035 (1998)
    OTHER SOURCE (OS):
                               CA 130:20710
                               2 (bases 1 to 1950)
Kasus-Jacobi,A.; Perdereau,D.; Burnol,A.-F.
REFERENCE:
    AUTHOR (AU):
    TITLE (TI):
                               Direct Submission
                               Submitted (03-JUL-1998) UPR 1524, CNRS, 9 rue Jules
    JOURNAL (SO):
                               Hetzel, Meudon 92190, France
FEATURES (FEAT):
                        Location
  Feature Key
                                                         Qualifier
/organism="Rattus norvegicus"
                    1..1950
source
                                                    /strain="wistar"
/db-xref="taxon:10116"
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/gene="Grb14"
                     1..1950
gene
CDS
                     70..1686
                                                    /note="signal transduction
                                                    protein; Grb7 family member; binds
                                                    the insulin receptor"
                                                    /codon-start=1
                                                    /product="molecular adapter
                                                    rGrb14'
                                                    /protein-id="AAC61478.1"
/db-xref="GI:3650500"
/translation="MTTSLQDGQSAAGRAGAQDS
                                                    PLAVQVCRVAQGKGDAQDPAQVPG
                                                    LHALSPASDATRRGAMDRRKAKDLEVQETPSIPN
                                                    PFPELCCSPLTSVLSAGLFPRSNS
                                                    RKKQVIKVYSEDETSRALEVPSDVTARDVCQLLI
                                                    LKNHYVDDNSWTLFEHLSHTGVER
                                                    TVEDHELLTEVLSHWVMEEDNKLYLRKNYAKYEF
                                                    FKNPMYFFPEHMVSFATEMNGDRS
                                                    LTQIPQVFLSSNTYPEIHGFLHAKEQGKKSWKKA
                                                    YFFLRRSGLYFSTKGTSKEPRHLQ
                                                    FFSEFSTSNVYMSLAGKKKHGAPTPYGFCFKPTK
                                                    AGGPRDLKMLCAEEDQSRMCWVTA
                                                    IRLLKYGMQLYQNYMHPSQARSACSSQSVSPMRS
                                                    VSENSLVAMDFSGQKTRVIDNPTE
                                                    ALSVAVEEGLAWRKKGCLRLGNHGSPTAPSQSSA
                                                    VNMALHRSQPWFHHRISRDEAQQL
                                                    ITRQGPVDGVFLVRDSQSNPRTFVLSMSHGQKIK
                                                    HFQIIPVEDDGEVFHTLDDGHTKF
                                                    TDLIQLVEFYQLNKGVLPCKLKHYCARMAV"
SEQUENCE (SEQ):
      1 gctggacccc agcctttctt cgctttcgcc tcgcggtcga tgactcccta gacccctqq
    61 cctacgatca tgaccacgtc cctgcaagat gggcagagcg ccgcgggccg ggcgggcgcc 121 caggactccc cgctggcagt gcaggtgtgc cgcgttgccc agggcaaggg agacgcccag
    181 gacceggete aggteceegg actgeacgeg etgteceegg ceteagatge gaccegeege
    241 ggtgccatgg acaggagaaa agcgaaagat ctggaagttc aggaaacgcc ttccattcct
    301 aacccettee etgagetetg etgiteteea ettacategg tgetgteage aggeetette
    361 cccagatcaa attcaaggaa gaaacaggtg attaaagttt acagcgagga tgagaccagc
   421 agagcgttag aggtgccag tgacgtcaca gcccgtgatg tctgccagct gttgatcctg
481 aagaaccact atgtcgacga caatagctgg accetttttg agcacctgtc tcacacaggc
541 gtagaaagga cagtggagga ccatgagctg ctgactgaag tgctgtctca ttgggtgatg
601 gaagaagata ataagctgta tcttagaaag aattatgcca aatagaatt ttttaagaac
661 ccaatgtatt tcttccaga gcacatgtgt tctttttcaaga cggtgacaga
   721 tecettacae agatecegea ggtgttttta ageteaaaea catateetga aateeatgge
   781 ttcctgcatg caaaggaaca ggggaagaag tcttggaaaa aagcttactt ttttctcaga
   841 agatcīggtī tataīītttc īācīaaāggc acatccaagg aaccacggca cttgcagtīt
   901 ticagigaat tcagcactag taatgittac atgicactgg caggcaaaaa aaagcatgga
   961 gcgccgactc cctatggatt ctgctttaag cctaccaaag caggagggcc ccgggacctg
  1021 aaaatgctgt gtgcagaaga agaccaaagc aggatgtgct gggtgaccgc cattagattg 1081 ctcaagtatg gcatgcagct ctaccagaat tatatgcatc catccaagc tagaagcgcc 1141 tgcagttctc agagcgtatc acccatgaga agcgtatcag agaattccct agtagcaatg 1201 gacttctcag gtcagaagac cagagtcata gacaacccca ctgaagccct ttcggttgcc
  1261 gttgaggaag gactcgcttg gaggaaaaaa ggatgtttac gcctggggaa tcatgggagt 1321 cccactgcgc cctctcagag ctctgctgtg aacatggctc tccaccggtc ccagccatgg 1381 tttcaccaca gaatttctag agatgaagct cagcagttga ttacccggca ggggcctgtg
```

```
1441 gatggagttt tcttggtacg ggatagtcag agtaacccca gaacttttgt actgtcaatg
  1501 agtcacggac aaaagataaa acactttcaa attatacccg tggaagatga tggtgaggtg
  1561 ticcacaccc tggatgatgg ccatacgaag ttcacagatc tcatccagct cgtggagttc
  1621 taccagetca acaagggggt cetteettge aagetgaage attactgtge taggatgget
  1681 gtttagccaa actgtctgtg actcgttaaa ctatggaaga tggaggatgc aaagaagaat
  1801 tcacaaggct ggaaacaaat catggtgaaa agaagattca cctgtgggtt acaaaaaaat
  1861 aggtcacgta ttgcaaatta gtgaagactt ggattcgtat tactctcgtt actttaaatt 1921 tattagttaa aattaaacct tattaaaaaa
L2
     ANSWER 150 OF 156
                            GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                         AI094433
                                       GenBank (R)
GenBank ACC. NO. (GBN): AI094433
GenBank VERSION (VER):
                         AI094433.1 GI:3433409
CAS REGISTRY NO. (RN):
                          392191-42-3
SEQUENCE LENGTH (SQL):
                         420
MOLECULE TYPE (CI):
                         mRNA; linear
DIVISION CODE (CI):
                          Expressed sequence tag
                         10 Nov 1998
ou87b07.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens
cDNA clone IMAGE:1634773 3' similar to TR:Q14449 Q14449
DATE (DATE)
DEFINITION (DEF):
                            ***GRB14*** . ;, mRNA sequence.
SOURCE:
                         human.
 ORGANISM (ORGN):
                         Homo sapiens
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                          Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                         Hominidae; Homo
NUCLEIC ACID COUNT (NA): 115 a
                                   75 c
                                           67 g
                                                  163 t
COMMENT:
     Contact: Robert Strausberg, Ph.D.
     Email: cgapbs-r@mail.nih.gov
     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
     Insert Length: 796
                          Std Error: 0.00
     Seg primer: -40m13 fwd. ET from Amersham
     High quality sequence stop: 277.
                         1 (bases 1 to 420)
REFERENCE:
   AUTHOR (AU):
                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
   TITLE (TI):
                         National Cancer Institute, Cancer Genome Anatomy
                         Project (CGAP), Tumor Gene Index
   JOURNAL (SO):
                         Unpublished (1997)
FEATURES (FEAT):
  Feature Key
                     Location
                                               Qualifier
/organism="Homo sapiens"
source
                 1..420
                                           /db-xref="taxon:9606"
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                                           /lab-host="DH10B"
                                           /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a
                                           modified polylinker; Site-1: Not
                                           I; Site-2: Eco RI; Equal amounts
                                           of plasmid DNA from five
                                           normalized libraries were mixed.
                                           and ss circles were made in vitro.
                                           Following HAP purification, this
                                           DNA was used as tracer in a
                                           subtractive hybridization
                                           reaction. The driver was PCR-amplified cDNAs from pools of
                                           5,000 clones made from the same 5
                                           libraries. The pools consisted of
                                           the following libraries and
                                           cloneIDs: Soares NbHSF pool 1:
                                           309384-310919, 323208-325895
                                           Soares Nb2HP pool 1:
                                           145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 soares Nb2HF8-9W
                                           pool 1: 758280-760583,
                                           772104-774407 Soares NbHPA pool 1:
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304776-306311, 320136-322823,

326280-326663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M.

normalization. Library constructed by Bento Soares and M. Fatima

```
Fatima Bonaldo.'
```

```
SEQUENCE (SEQ):
      f 1 cctaaggttt aattttaact aatgaatttt aaatgatgaa tf gtaaf agtca f atccf agtct
   61 ttgcttattt gcaatgcaca aactatttt ttgtaacttg caggtgaaat acattctttt 121 cacatgataa cgttttcgcc cttatttatg gtcttttatt attttcttg agtccttttc 181 cttcaatagt ttaataagtc acttctggct tgtctagaga gcaatcctag cacaataatg 241 tttcaacttg caaggaagaa cgcccttatt gagttgatag aactccacca gctgtattag
    301 atctgtaaať cttgtgtggc catcatccag tgtgtggaac atttcaccgt catcttctac
    361 tggtataatt tgaaagtgct ttattttttg tccatgactc attgacagta cgaaagtttt
L2
      ANSWER 151 OF 156
                                 GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                              AA917917
                                               GenBank (R)
GenBank ACC. NO. (GBN): AA917917
GenBank VERSION (VER):
                              AA917917.1 GI:3057807
CAS REGISTRY NO. (RN):
                              206814-02-0
SEQUENCE LENGTH (SQL):
                              497
MOLECULE TYPE (CI):
                              mRNA; linear
DIVISION CODE (CI):
                              Expressed sequence tag
DATE (DATE):
                              10 Jun 1998
DEFINITION (DEF):
                              ol76g09.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone
                              IMAGE: 1535584 3' similar to TR: Q14449 Q14449
                                 ***GRB14***
                                                 . ;, mRNA sequence.
SOURCE:
 ORGANISM (ORGN):
                              Homo sapiens
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                              Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                              Hominidae; Homo
NUCLEIC ACID COUNT (NA): 136 a
                                          95 c
                                                   79 g
                                                            187 t
COMMENT:
      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs-r@mail.nih.gov
      Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
      Emmert-Buck, M.D., Ph.D.
       cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      www-bio.llnl.gov/bbrp/image/image.html
      Insert Length: 664
                                 Std Error: 0.00
      Seq primer: -40m13 fwd. ET from Amersham
      High quality sequence stop: 440.
REFERENCE:
                                 (bases 1 to 497)
   AUTHOR (AU):
                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
   TITLE (TI):
                              National Cancer Institute, Cancer Genome Anatomy
                              Project (CGAP), Tumor Gene Index
Unpublished (1997)
   JOURNAL (SO):
FEATURES (FEAT):
  Feature Key
                         Location
                                                        Oualifier
source
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                                                   /clone-lib="NCI-CGAP-Kid3"
                                                   /lab-host="DH10B'
                                                  /note="Organ: kidney; Vector:
pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site-1: Not
I; Site-2: Eco RI; 1st strand cDNA
                                                   was primed with a Not I -
                                                   oligo(dT) primer, double-stranded CDNA was ligated to Eco RI
                                                  adaptors (Pharmacia), digested with Not I and cloned into the Not
                                                   I and Eco RI sites of the
                                                  modified pT7T3 vector. mRNA
source: 2 pooled kidneys. Library
went through one round of
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SEQUENCE (SEQ):
      1 cattititic ctaaggitta attitaacta atgaatitta aatgatgaat gtaaagtcaa
     61 tccaagtett tgettätttg caatgeacaa actattttt tgtäaettge äggtgäaata
   121 cattettte acatgataat gttttegee ttatttatgg tetttatta ttttettga
181 gtcetttee tteaatagtt taataagtea ettetggett gtetagagag caateetage
241 acaataatgt tteaacttge aaggaagaae geeettattg agttgataga acteeaceag
301 etgtattaga tetgtaaate ttgtgtggee ateateeagt gtgtggaaca ttteaeegte
361 atettetaet ggtataattt gaaagtgett tattteetgt eeatgaetea ttgaeagtae
    421 gaaagttttg gggttactct gactatcccg taccaagaaa actcatccac aagtccttgc
    481 tgaataatca atcgctg
L2
      ANSWER 152 OF 156
                                 GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                               AA684351
                                               GenBank (R)
GenBank ACC. NO. (GBN): AA684351
GenBank VERSION (VER): AA684351
                               AA684351.1 GI:2670937
CAS REGISTRY NO. (RN): SEQUENCE LENGTH (SQL):
                               200792-61-6
                               503
MOLECULE TYPE (CI):
                               mRNA; linear
DIVISION CODE (CI):
                               Expressed sequence tag
DATE (DATE):
                               9 Dec 1997
DEFINITION (DEF):
                               vm69d04.s1 Knowles Solter mouse 2 cell Mus musculus
                               cDNA clone IMAGE:1003495 5' similar to TR:014449 014449
                                 ***GRB14*** . ;, mRNA sequence.
SOURCE:
                               house mouse.
 ORGANISM (ORGN):
                               Mus musculus
                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                               Euteleostómi; Mammália; Euthéria; Rodentia;
Sciurognathi; Muridae; Murinae; Mus
NUCLEIC ACID COUNT (NA): 127 a 121 c
                                                    135 g
COMMENT:
      Contact: Marra M/Mouse EST Project
      WashU-HHMI Mouse EST Project
      Washington University School of MedicineP
      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
      Tel: 314 286 1800
Fax: 314 286 1810
      Email: mouseest@watson.wustl.edu
      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
      Possible reversed clone: similarity on wrong strand
      High quality sequence stop: 459.
REFERENCE:
                               1
                                 (bases 1 to 503)
   AUTHOR (AU):
                              Marra, M.; Hillier, L.; Allen, M.; Bowles, M.; Dietrich, N.;
                              Dubuque,T.; Geisel,S.; Kucaba,T.; Lacy,M.; Le,M.;
                              Martin, J.; Morris, M.; Schellenberg, K.; Steptoe, M.; Tan, F.; Underwood, K.; Moore, B.; Theising, B.; Wylie, T.; Lennon, G.; Soares, B.; Wilson, R.; Waterston, R. The WashU-HHMI Mouse EST Project
   TITLE (TI):
   JOURNAL (SO):
                              Unpublished (1996)
FEATURES (FEAT):
  Feature Key
                       Location
                                                        Qualifier
source
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                                                   /strain="B6D2 F1/J"
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                                                   cell"
                                                   /tissue-type="embryo"
/dev-stage="2-cell"
                                                   /lab-host="DH10B"
                                                   /note="Organ: embryo; Vector:
                                                   pBluescribe (modified); Site-1:
                                                   MluI; Site-2: SalI; Cloned
                                                   cDNAs were cloned into the
                                                   MluI/SalI sites of a modified
```

pBluescribe vector using

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SEQUENCE (SEQ):
      1 ttccctagta gcaatggact tctcaggtga gaagagcaga gtcatagaca accccactga
   61 agcgctttcg gttgctgttg aggaaggcct cgcgtggagg aaaaaaggct gtttacgcct 121 ggggaatcac ggaagcccca gtgcccctc ccagagctct gctgtgaaca tggctctcca 181 tcggtcccaa ccatggttc accacagaat ttccagagat gaggctcagc ggctgatcat 1241 tcggcagggg cctgtggatg gagtttctt ggtacgggat agtcagagta accccagaac 1241 tcggcagggg tcaatgagtc atggacaaaa gataaaacac tatcaaatta tacccgtaga 125 agatgatggt gagctgttc atactctgga tgatggccat acgaagttca cagacctcat 125 ccacatagt gagctgttca agatgacata acgaagttca acgaagttca cagacctcat 125 ccacatagta gagctgttca agatgacata acgaagttca cagacctcat 125 ccacatagta gagctgttca agatgacata acgaagttca cagacataa
    421 ccagctggtg gagttctacc agctcaacag gggggtcctt ccttgcaagc tgaagcatta
   481 ctgtgctagg atggctgttt agc
L2
      ANSWER 153 OF 156
                                 GENBANK.RTM. COPYRIGHT 2004 on STN
LOCUS (LOC):
                               HSU69276
                                               GenBank (R)
GenBank ACC. NO. (GBN): U69276
GenBank VERSION (VER):
                               U69276.1 GI:1546834
CAS REGISTRY NO. (RN):
                               181109-72-8
SEQUENCE LENGTH (SQL):
                               2504
MOLECULE TYPE (CI):
                              mRNA; linear
DIVISION CODE (CI):
                               Primates
DATE (DATE):
                               17 Sep 1996
DEFINITION (DEF):
                               Human hGrbIRbeta/hGrb10 (GRBIRbeta/GRB10) mRNA.
                               complete cds.
SOURCE:
                               human.
 ORGANISM (ORGN):
                               Homo sapiens
                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                               Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
                              Hominidae; Homo
                                          652 c
NUCLEIC ACID COUNT (NA): 639 a
                                                    654 q
                                                              555 t 4 others
REFERENCE:
                                 (bases 1 to 2504)
   AUTHOR (AU):
                               Frantz, J.D.; Giorgetti-Peraldi, S.; Ottinger, E.A.;
                               Shoelson, S.E.
   TITLE (TI):
                              Human GrbIRbeta/Grb10: Splice Variants of an Insulin
                              and Growth Factor Receptor-Binding Protein with PH and
                              SH2 Domains
   JOURNAL (SO):
                              Unpublished
                              2 (bases 1 to 2504)
Frantz,J.D.; Giorgetti-Peraldi,S.; Ottinger,E.A.;
REFERENCE:
   AUTHOR (AU):
                              Shoelson, S.E.
   TITLE (TI):
                              Direct Submission
   JOURNAL (SO):
                              Submitted (04-SEP-1996) Research Division, Joslin
                              Diabetes Center, One Joslin Place, Boston, MA 02215,
                              USA
FEATURES (FEAT):
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                         Location
                                                        Qualifier
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                                                   /tissue-type="cerebellum and
                                                   skeletal muscle"
gene
                    1..2504
                                                   /gene="GRBIRbeta/GRB10"
CDS
                                                   /gene="GRBIRbeta/GRB10"
                    288..1898
                                                   /note="signal transduction protein
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                                                   a potential SH3 domain interaction
                                                   site; insulin receptor binding
                                                  protein, binds the insulins, PDGF, and EGF receptors; splice variant of hGrbIR; member of the
                                                   Grb7/Grb10/Grb14 family"
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                                                   /product="hGrbIRbeta/hGrb10"
                                                   /protein-id="AAB08431.1
                                                   /db-xref="GI:1546835
                                                   /translation="MNASLESLYSACSMQSDTVP
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                                                   VSPRQRVQRSQPVHILAVRRLQEEDQQFRTSSLP
                                                   AIPNPFPELCGPGSPPVLTPGSLP
                                                   PSQAAAKQDVKVFSEDGTSKVVEILADMTARDLC
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QTQLLQNFLNSSSCPEIQGFLHVKELGKKSWKKL YVCLRRSGLYCSTKGTSKEPRHLQ LLADLEDSNIFSLIAGRKQYNAPTDHGLCIKPNK VRNETKELRLLCAEDEQTRTCWMT AFRLLKYEMLLYQNYRIPQQRKALLSPFSTPVRS VSENSLVAMDFSGQTGRVIENPAE AQSAALEEGHAWRKRSTRMNILGSQSPLHPSTLS TVIHRTQHWFHGRFSREESHRIIK QQGLVDGLFLLRDSQSNPKAFVLTLCHHQKIKNF QILPCEDDGQTFFSLDDGNTKFSD LIQLVDFYQLNKGVLPCKLKHHCIRVAL"

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     181 cacctcgcag tcaacaagac ccggcaggac caggactccc cgcacagtct gaccgacttg
     241 cgaatcacca ggaggatgat gtggacctgg aagccctggt gaacgatatg aatgcatccc 301 tggagagcct gtactcggcc tgcagcatgc agtcagacac ggtgcccctc ctgcagaatg gccagactgc ccgcagccag cctcgggctt caggccctc tcggtccatc cagccacagg 421 tstaccaca
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     481 třcaggagga agaccagcag triagaacct cătctčtgcc ggccatcccc aatcčititc
     541 ctgaactctg tggccctggg agcccccctg tgctcacgcc gggttcttta cctccgagcc
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     661 agattetage agacatgaca gecagagace tgtgecaatt getggtttae aaaagteact
     721 gtgtggatga caacagctgg acactagtgg agcaccaccc gcacctagga ttagagaggt
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   1201 gcataaagcc aaacaaagtc aggaatgaaa ctaaagagct gaggttgctc tgtgcagagg
   1261 acgagcaaac caggacgtgc tggatgacag cgttcagact cctcaagtat gaaatgctcc
   1321 tttaccagaa ttaccgaatc cctcagcaga ggaaggcctt gctgtccccg ttctcgacgc
   1381 cagtgcgcag tgtctccgag aactccctcg tggcaatgga tttttctggg caaacaggac
   1441 gcgtgataga gaatccggcg gaggcccaga gcgcagccct ggaggagggc cacgcctgga
1501 ggaagcgaag cacacggatg aacatcctag gtagccaaag tcccctccac ccttctaccc
1561 taagtacagt gattcacagg acacagcact ggtttcacgg gaggttctcc agggaggaat
1621 cccacaggat cattaaacag caagggctcg tggatgggct ttttctcct cgtgacagcc
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   1921 agactggagg aagtgaacac tggagtgaag aagcggtctg tgcgttggtg aagaacacac
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   2101 ccctctgcgt cggncaaatt ggggagggca tggaagatcc agcggaaagt tgaaaataaa 2161 ctggaatgat catcttggct tgggccgctt aggaacaaga accggagaga agtgattgga
   2221 aatgaactet tgecetggaa taatettgae aattaaaaet gatatgtta ettttttgt
2281 attgateaet tttttggaet eettetttgt ttteaatatt gtatteagee tattgtagga
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2401 aactgaatat gggtccccaa atgttcccag agggtcctcc acaacctctg ncgactacca
   2461 cggtgtngga ttcagctccc aaatgacaaa cccagncctt ccca
L2
       ANSWER 154 OF 156
                                         GENBANK.RTM.
                                                               COPYRIGHT 2004 on STN
LOCUS (LOC):
                                      HUMGRB14R
                                                            GenBank (R)
GenBank ACC. NO. (GBN): L76687
GenBank VERSION (VER):
                                      L76687.1 GI:1369836
CAS REGISTRY NO. (RN):
                                      391791-70-1
SEQUENCE LENGTH (SQL):
                                      2376
MOLECULE TYPE (CI):
                                     mRNA; linear
DIVISION CODE (CI):
                                      Primates
```

6 May 1998

human.

Homo sapiens

Homo sapiens

Hominidae; Homo 631 a 652 c

(bases 1 to 2376)

Grb14

583 a

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;

510 t

Daly,R.J.; Sanderson,G.M.; Janes,P.W.; Sutherland,R.L.

Cloning and characterization of ***GRB14*** , a

mRNA, complete cds.

DATE (DATE):
DEFINITION (DEF):

ORGANISM (ORGN):

AUTHOR (AU):

TITLE (TI):

NUCLEIC ACID COUNT (NA): 631 a

SOURCE:

REFERENCE:

novel member of the GRB7 gene family

JOURNAL (SO): J. Biol. Chem., 271 (21), 12502-12510 (1996) OTHER SOURCE (OS): CA 125:27254

FEATURES (FEAT):

Feature Key	Location	Qualifier
_	Location +====================================	
3'UTR	21642376	TEALSVAVEEGLAWRKKGCLRLGTHGSPTASSQS SATNMAIHRSQPWFHHKISRDEAQ RLIIQQGLVDGVFLVRDSQSNPKTFVLSMSHGQK IKHFQIIPVEDDGEMFHTLDDGHT RFTDLIQLVEFYQLNKGVLPCKLKHYCARIAL" /gene="Grb14"

SEQUENCE (SEQ):

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- 2281 ttacaaaaa atagtttgtg cattgcaaat aagcaaagac ttggattgac tttacattca 2341 tcatttaaaa ttcattagtt aaaattaaac cttagg L2 ANSWER 155 OF 156 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN 2004:13636 AGRICOLA ΑN IND43619263 DN ΤI Improved glucose homeostasis and enhanced insulin signalling in ***Grb14*** -deficient mice. Cooney, G.J.; Lyons, R.J.; Crew, A J.; Jensen, T.E.; Molero, J.C.; ΑU Mitchell, C.J.; Biden, T.J.; Ormandy, C.J.; James, D.E.; Daly, R.J. ΑV DNAL (QH506.E46) EMBO journal, p. 582-593 ISSN: 0261-4189 50 NTE Includes references Article DT Non US FS English LA L2 ANSWER 156 OF 156 CONFSCI COPYRIGHT 2004 CSA on STN ΑN 1999:27349 CONFSCI 99-039843 DN ***Grb14*** TI Novel FGF signaling pathway u binds to FGF receptor 1 ΑU Reilly, J.F.; Mickey, G.; Maher, P.A. CS SO
- AU Reilly, J.F.; Mickey, G.; Maher, P.A.

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 American Society for Cell Biology, 9650 Rockville Pike, Bethesda, MD 20814, USA; phone: (301) 530-7153; fax: (301) 530-7139; email: ascbinfo@ascb.org; URL: www.ascb.org/ascb/, Abstracts available. Price \$45. Paper No. 1365.

 Meeting Info.: 984 0478: 38th American Society for Cell Biology Annual Meeting (9840478). San Francisco, CA (USA). 12-16 Dec 1998. ASCB, Bio-Rad, Genentech, Jeol USA, Johnson & Johnson, Leica, Leadership Alliance, Mark-Rambar Family Foundation.

 DT Conference
- FS DCCP LA English
- STN INTERNATIONAL LOGOFF AT 15:32:52 ON 09 JUL 2004